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10	20	30	40	50	60	70	80	90
GACGGATCGG	GAGATCTCT	AGGTGACCTG	AGGGCGCCG	GCTTCGAATA	CCCATGGTTT	TAATTATTT	TTATTTTT	
CTGCTAGCC	CTCTAGACGA	TCCACTGGAC	TCCGGCGGCC	CGAAGCTTAT	CGGTCTCAT	GGAAAAAAA	ATTTAAATAA	AATAAAATAA
100	110	120	130	140	150	160	170	180
TTTGAGATGG	AGTTTGGCGC	CGATCTCCCG	ATCCCCCTATG	GTCGACTCTC	AGTACAATCT	GCTCTGATGC	CCGATAGTTA	AGCCAGTATC
AAACTCTACC	TCAAACCGGG	GCTAGAGGGC	TAGGGGATAC	CAGCTGAGAG	TCATGTTAGA	CGAGACTACG	GGGTATCAAT	TCCGTCATAG
190	200	210	220	230	240	250	260	270
TGCTCCCTGC	TGTGTGTGTTG	GAGGTGCGCTG	AGTAGTGGCG	GAGGAAAATT	TAAGCTACAA	CAAGGCAAGG	CTTGACOGAC	AATGCGATCA
ACGAGGGACG	AACACACAC	CTCCOAGCGAC	TCATCACCGG	CTCGTTTAA	ATTCGATGTT	GTTCCGTTCC	GAACGGCTG	TTAACGTRACT
280	290	300	310	320	330	340	350	360
AGAATCTGCT	TAGGGTTAGG	CGTTTTCGCG	TGCTTCGCGA	TGTAACGGCC	AGATATAACG	GTGACATTTG	ATTATTGACT	AGTTATTAAAT
TCTTAGACGA	ATCCCAATCC	GCAAAACGCG	ACGAAGGCT	ACATGCCCGG	TCTATATGCG	CAACTGTAAC	TAATAACTGA	TCAATAATTA
370	380	390	400	410	420	430	440	450
AGTAATCAAT	TACGGGGTCA	TTAGGTTCTATA	GCCCCATATAT	GGAGTTCCGC	GTTACATAAC	TTACGGTAA	TGGCCCGCCT	GGCTGACCGC
TCATTAAGTAA	ATGCCCTAAGT	AATCAAGTAT	CGGGTATATA	CCTCAAGGGG	CAATGTATTG	AATGCCATT	ACCGGGCGGA	CCGACTCGCG
460	470	480	490	500	510	520	530	540
CCAACGACCC	CCGCCCATTG	ACGTCAATAA	TGACGTTATG	TCCCACATAGA	ACGCCAATAG	GGACTTTCCA	TTGACGTCAA	TGGTGGACT
GGTTGCTGGG	GGGGGTAAAC	TGGCACTTATT	ACTGCATACA	AGGGTATCAT	TGCGGTTATC	CCTGAAAGGT	AACTGCAGTT	ACCCACCTGA
550	560	570	580	590	600	610	620	630
ATTACGGTA	AACTGCCAC	TTGGCAAGTAC	ATCAAGTGT	TCATATGCCA	AGTACGCC	CTATTGACG	CAATGACGGT	AAATGGCCCC
TAATGCCAT	TTGACGGGTG	AACCGTCATG	TAGTTACAT	AGTATACGGT	TCATGCCGGG	GATAACTGCA	GTTACTGCCA	TTTACCGGGC
640	650	660	670	680	690	700	710	720
CCTGGCATT	TGCCCCAGTAC	ATGACCTTAT	GGGACTTTCC	TACTTGGCG	TACATCTACG	TATTAGTCA	CGCTATPACC	ATGTCATGCC
GGACCGTAAT	ACGGGTCACTG	TACTGGAAATA	CCCTGAAAGG	ATGAAACGGTC	ATGTAATGTC	ATAATCAGTA	GGGATAATGG	TACCACTACG
730	740	750	760	770	780	790	800	810
GGTTTGGCA	GTACATCAAT	GGGGGTGGAT	AGCGGGTTGA	CTCACGGGGA	TTTCCAAAGTC	TGCCACCCAT	TGACGTCAAAT	GGGAGTTGT
CCAAAACCGT	CATGTCAGTAA	CCGGCACCTA	TCGCCAAACT	AGTGTGCCCT	AAAGGTTCA	AGGTGGGGTA	ACTGCAGTTA	CCCTCAAAACA
820	830	840	850	860	870	880	890	900
TTGGCACCA	AAATCAACGG	GACTTCCAA	AATGTCGTA	AACTCCGCC	CCATTGACGC	AAATGGGGGG	TAGGGGTGTA	CGGTGGGAGG
AAACCGTGGT	TTTACGGATT	CTGMAAAGGT	TTACAGCATT	CTGAGGGGG	GGTAACCTGCG	TTAACCCGCC	ATCCGCACAT	GCCACCCCTCC

FIGURE 14A
(SEQ ID NO. 10)

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910	920	930	940	950	960	970	980	990
TCTATATAAG	CAGAGGCTCTC	TGGGCTAACTA	GAGAACCCAC	TGCTTACTGG	CTTATCGAAA	TTAATACGAC	TCACTATAGG	GAGCCCCAAG
AGATATATTG	GTCTCGAGG	ACCGATTGAT	CTCTTGGGTG	ACGAATGACC	GRATAGCTT	AATTATGCTG	AGTGATATCC	CTCTGGGTTTC
1000	1010	1020	1030	1040	1050	1060	1070	1080
CTTGGTACCA	ATTTAAATG	ATATCTCCTT	AGGTCTCGAG	TCTCTAGATA	ACCGGTCAAT	CGATTGGAAT	TCTTGGGCC	GCTTGCTAGC
GAACCATGGT	TAATTTAAC	TATAGAGGAA	TCCAGAGCTC	AGAGATCTAT	TGGCCAGTTA	GCTAACCTA	AGAACGCCGG	CGAACGATCG
1090	1100	1110	1120	1130	1140	1150	1160	1170
CACCATGGAG	TGTGGTTAA	GCTTGGTCCT	TCCTTGTCTT	TGTTTAAAAA	GGTGTCCAGT	GTGAAGTGA	TCTGGTGGAG	TCTGGGGAG
GTGGTACCTC	ACACCAATT	CGAACCCAGGA	AGGAACAGGA	ACAAATTTT	CCACAGGTCA	CACTTCACTT	AGACCAACTC	AGACCCCTC
1180	1190	1200	1210	1220	1230	1240	1250	1260
GCTTAGTGCA	GCCTGGAGGG	TCCCTGAAAG	TCTCCTGTGT	AACCTCTGGA	TTCACTTCA	GTGACTATTA	CATGTATTCG	GTTGCCAGA
CGAACATCACGT	GGACCTCCC	AGGAACTTTC	AGGGACACA	TGGAGACCT	AAGTGAAGT	CACTGATAAT	GTACATAAAC	CAAGGGTCT
1270	1280	1290	1300	1310	1320	1330	1340	1350
CTCCAGAGAA	GAGGCTGGAG	TGGCTCGCAT	ACATTAGTCA	AGGTGGTGTAT	ATAACCGACT	ATCCAGACAC	TGTAAAGGGT	CGATTCACCA
GAGGTCTCTT	CTCCGACCTC	ACCCAGGTA	TGTAATCAGT	TCCACCACTA	TATTGGCTGA	TAGGTCTGTG	ACATTTCCCA	GCTAAGTGGT
1360	1370	1380	1390	1400	1410	1420	1430	1440
TCTCCAGAGA	CAATGCCAAG	AACACCCCTGT	ACCTGCAAAT	GAGCGTCTG	AAGTCTGAGG	ACAOAGCCAT	GTATTACTGT	GCAAGAGGCC
AGAGGTCTCT	GTACGGTTTC	TTGTGGGACA	TGGACGTTA	CTCGGCGAGAC	TTCAAGCTCC	TGTGTGGTA	CATAATGACA	CGTTCTCCGG
1450	1460	1470	1480	1490	1500	1510	1520	1530
TGGACGACGG	GGCCTGGTT	GCTTACTGGG	GCCAAAGGAC	TCTGGTCAGC	GTCTCTGTAG	CTAGGACCAA	GGGCCCAATCG	GTCTTCCCC
ACCTGCTGCC	CGGGACCAA	CGAATGACCC	CGGTTCCCTG	AGACCACTGC	CAGAGACATC	GATGTTGGTT	CCGGGGTACG	CAGAAGGGG
1540	1550	1560	1570	1580	1590	1600	1610	1620
TGGCACCCCTC	CTCCAAGAGC	ACCTCTGGG	GCACAGGGC	CCTGGGCTGC	CTGGTCAGG	ACTACTTCCC	CGAACCCGGT	ACGGTGTCTGT
ACCGTGGGAG	GAGGTCTCG	TGGAGACCCC	CGTGTGCGCG	GGACCCGACG	GACCAGTTC	TGATGAAGGG	GCTTGGCCAC	TGCCACAGCA
1530	1640	1650	1660	1670	1680	1690	1700	1710
GGAACTCAGG	GGCCCTGACC	AGGGCGTGC	ACACCTTCCC	GGCTGTCCCTA	CAGTCCTOAG	GACTCTACTC	CCTCAGGCAAC	GTGGTCACCG
CCCTGAGTCC	GGGGGACTGG	TGCGCGCAGC	TGTGGAGGG	CCGACAGGAT	GTCAAGGAGTC	CTGAGATGAG	GGAGTCGTG	CACCACTGGC
1720	1730	1740	1750	1760	1770	1780	1790	1800
TGCCCTCCAG	CAGCTGGGC	ACCCAGACCT	ACATCTGCAA	CCTGAATCAC	AAAGCCAGCA	ACACCAAGGT	GGACAAGAAA	GTTGGTGAGA
ACGGGAGGTC	GTGGAACCCG	TGGCTCTGGA	TGTAGACGTT	GCACCTAGTG	TGTGGGTCTT	CCCTGGTCCA	CCCTGGTCTT	CAACCACTCT

FIGURE 14B
(SEQ ID NO. 10)

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1810	1820	1830	1840	1850	1860	1870	1880	1890
GGCCAGCACA	GGGAGGGAGG	GTTGTCGTG	GAAGGCCAGGC	TCAGCGCTCC	TGCCCTGGACG	CATCCCCGGCT	ATGCCAGCCC	AGTCAGGGC
CGGGTCTGT	CCCTCCCTTC	CACAGACGAC	CTTCGGTCG	AGTCGGAGG	ACGGACCTGC	GTAGGGCCGA	TACGTCGGGG	TCAGGTCCCC
1900	1910	1920	1930	1940	1950	1960	1970	1980
AGCAAGGGAG	GCCCCGGCTG	CCTCTTCACC	CGGAGGGCCTC	TGCCCGCCCC	ACTCATGCTC	AGGGAGAGGG	TCTTCTGGCT	TTTTCCCCAG
TGTTTCCGTC	CGGGGGAGAC	GGAGAAAGTGG	GCCTCCGGAG	ACGGGGGGGG	TGAGTACGAG	TCCCCTCTCC	AGAAGACCGA	AAAAGGGTC
1990	2000	2010	2020	2030	2040	2050	2060	2070
GCTCTGGCA	GGCACAGGGT	AGGTGCCCT	AACCCAGGGC	CTGCACACAA	AGGGCAGGT	GCTGGGCTCA	GACCTOCCAA	GAGCCATATC
CGAGAACCCGT	CCGGTCTCGA	TCCACGGGAA	TTCGGTCTGG	GAACGTGTGTT	TCCCCGTCCA	CGACCCGGAGT	CTGGACGGTT	CTCGGTATAG
2080	2090	2100	2110	2120	2130	2140	2150	2160
CGGGAGGACC	CTGCCCTCTGA	CCTAAGCCCC	CCCCAAAGGC	CAAACCTCTCC	ACTCCCTCA	CTCGGACACC	TTCTCTCCCTC	CCAGATTCCA
GCCCTCTCTGG	GACGGGGACT	GGATTGGGGT	GGGGTTTCG	GTTTGAGAGG	TGAGGGAGTC	GAGCCTGTTG	AAGAGGGAG	GGTCTAAGGT
2170	2180	2190	2200	2210	2220	2230	2240	2250
GTAACCTCCA	ATCTTCTCTC	TGCAAGAGCCC	AAATCTTGTG	ACAAAACCTCA	CACATGCCCA	CCGTGCCAG	GTAAGGCCAGC	CCAGGCCTCG
CATTGAGGGT	TAGAAGAGAG	ACGTCTCGGG	TTTAGAACAC	TGTTTTGAGT	GTGTAACGGGT	GGCACGGGTG	CATTGGGTG	GGTCGGAGC
2260	2270	2280	2290	2300	2310	2320	2330	2340
CCCTCAGGCT	CAAGGGGGAA	CAGGTGCCCT	AGAGTAGGCT	GCATTCAGGG	ACACACCAAG	TGGGTACCAA	CATGTCGGGA	GCCACATCGA
GGGAGGTCGA	GTTCGGCCCT	GTCCACGGGA	TCTCATCGGA	CGTAGGTCCC	TGTGTGGTGC	ACCCATGGTT	GTACAGGCC	CGGTGTACCT
2350	2360	2370	2380	2390	2400	2410	2420	2430
CAGAGGCCG	CTCGGGCCAC	CTCTCTGCCCT	GAGAGTGAAC	CTCTCTGTC	TACAGGGCAG	CCCCGGAGAC	CACAGGTGTA	
GTCTCGGGC	GAAGCGGGTG	GGAGACGGGA	CTCTCACTGG	CGACATGGTT	GGAGACAGGG	ATGTCCCGTC	GGGGCTCTTG	GTGTCACAT
2440	2450	2460	2470	2480	2490	2500	2510	2520
CACCCCTGCC	CCATCCGGGG	ATGAGCTGAC	CAAGAACGAG	GTCAGCCTGA	CTCTGCTGCT	CAAAGGCTTC	TATCCAGGG	ACATCGCCGT
GTGGGACGGG	GTAGGGGCC	TACTCGACTG	GTTCCTGGTC	CACTGGACT	GGACGGACCA	GTTTCCGAAG	ATAGGGTCGC	TGTAGGGCA
2530	2540	2550	2560	2570	2580	2590	2600	2610
GGAGTGGAG	AGCAATGGGC	AGCCGGAGAA	CAACTACAAG	ACCAAGCCTC	CCGTGCTGGA	CTCCGACGGC	TCCTTCTCC	TCTACAGCAA
CCTCACCCCTC	TCGGTTACCGG	TCGGCCTCTT	GTGTAATGTC	TGGTGGGGAG	GGCACCGACT	GAGGTGGGG	AGGAAGAAGG	AGATGTCGTT
2620	2630	2640	2650	2660	2670	2680	2690	2700
GCTCACCGTG	GACAAGAGCA	GGTGGCAGCA	GGGAAACGGC	TTCTCATGCT	CCGTGATGCA	TGAGGCTCTG	CACAACCACT	ACACGCCAGAA
CGAGTGGCAC	CTGTTCTCGT	CCACCGCTCT	CCCCCTTGGAG	AAGAGTACGA	GGCACACTAGT	ACTCCGAGAC	GTGTGGTGTG	TGTGGGTCTT

FIGURE 14C
(SEQ ID NO. 10)

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2710	2720	2730	2740	2750	2760	2770	2780	2790
GAGCCTCTCC	CTGTCCTCCGG	GTAATGAGT	GCGACGGCG	GCAAGCCCC	GCTCCCGGG	CTCTCGGGT	CGCACAGGA	TGCTGGCAC
CTCGAGAGG	GACAGAGCC	CATTACTCA	CGCTGGGGC	CGTTCGGGG	CGAGGGGCC	GAGAGGCCA	GGTAGGCCA	ACGAAACCGTG
2800	2810	2820	2830	2840	2850	2860	2870	2880
GTACCCCTTG	TACATACTTC	CGGGGGCCC	ACCATGGAAA	TAAAGCACCC	AGCGCTGGCC	TGGGCCCTG	CGAGACTGTG	ATGGTTCTTT
CATGGGGAC	ATGTATGAG	GGCCCGGGGG	TCGTACCTT	ATTCGTGGG	TCGGGACGGG	ACCCGGGAC	GCTCTGACAC	TACCAAGAAA
2890	2900	2910	2920	2930	2940	2950	2960	2970
CCACGGGTCA	GGCGAGTCT	GAGGCCTGAG	TGGCATGAGG	GAGCCAGAGC	GGGTCCCACT	GTCCCCACAC	TGGCCAGGC	TGTCAGGGTG
GGTCCCCAGT	CCGGCTCAGA	CTCCGGACTC	ACCGTACTCC	CTCCGTCTG	CCAGGGTGTG	ACGGGGTCCG	ACACGGTCCAC	
2980	2990	3000	3010	3020	3030	3040	3050	3060
TGCCCTGGCC	CCCTAGGGTG	GGGCCTAGCC	AGGGCTGCC	CTCGGAGGG	TGGGGGATT	GCCAGCGTGG	CCCTCCCTCC	AGCAGCACCT
ACGAACCCGG	GGGATCCAC	CCCGAGTCGG	TCCCCGACGG	GAGCCGTCCC	ACCCCCCTAAA	CGGTGCGACC	GGGAGGGAGG	TCGTCGTGGA
3070	3080	3090	3100	3110	3120	3130	3140	3150
GCCCTGGGCT	GGGCACAGGG	AAGCCCTAGG	AGGCCCTGGG	GACAGACACA	CAGGCCCTGC	CTCTGTAGGA	GACTGTCTG	TTCCTGTGAGC
CGGGACCCGA	CCCCGGTGCC	TTGGGGATCC	TCGGGGACCC	CTGTCTGTGT	GTCGGGGAGC	GAGACATCTT	CTGACAGGAC	AAGACACTCG
3160	3170	3180	3190	3200	3210	3220	3230	3240
GCCCCCTGTC	TCCCCGACCTC	CATGCCCACT	CGGGGCCATG	CCTAGTCCAT	GTCGGTAGGG	ACAGGGCCCTC	CCTCACCCAT	CTACCCCCAC
CGGGGACAGG	AGGGCTGGAG	GTACGGGTGA	GCCCCCGTAC	GGATCAGGTA	TCTCGGGAG	GGAGTGGGTA	GATGGGGGTG	
3250	3260	3270	3280	3290	3300	3310	3320	3330
GGCACTAAC	CTGGGCTGCC	CTGCCCAAGCC	TGGCACCCGC	ATGGGACAC	RACCGACTCC	GGGGACATGC	ACTCTCGGGC	CCTCTGGAGG
CCGTRATTGG	GGACCCGACGG	GACGGGTCTGG	AGCGTGGCG	TACCCCTGTG	TTGGCTGTAGG	CCCCCTGTACG	TGAGAGCCCC	GGACACCTCC
3340	3350	3360	3370	3380	3390	3400	3410	3420
GACTGGTGCA	CATGCCACA	CACACACTCA	GCCCCAGACCC	GTTCACAAAAA	CCCCGGACTG	GGGTGGGGC	GCCACACGGC	CACCAACAC
CTGACCACT	CTACGGGTGT	GTGTGTGAGT	CGGGTCTCGG	CAAGTGTGTT	GGGGCTGTAC	TCCRAACGGG	CGCTGTGCG	GTGGGTGTCG
3430	3440	3450	3460	3470	3480	3490	3500	3510
ACACGTGCAC	GCCTCACACA	CGGAGCCTCA	CCCCGGCGAA	CTGCACAGCA	CCCGAGACAG	TCGGCACACGT	GAACACCTCCT	
TGTGACGTG	CGGAGTGTGT	GGCTTCGGAGT	GGGCCCGGTT	GACGTGTGCGT	GGGTCTGGTC	TGTTTCCAGG	AGCGTGTGCA	CTTGTGAGGA
3520	3530	3540	3550	3560	3570	3580	3590	3600
CGGACACAGG	CCCCCACGAG	CCCCACGGG	CACCTCAAGG	CCCCAGAGCC	TCTCGGGCAGC	TTCTCCACAT	GCTGACCTGC	TCAGACAAAC
GCCCTGTGTC	GGGGGTGCTCC	GGGGGGGCC	GTGGAGTTCC	GGGTGCTCGG	AGAGCCGTGTA	CGACTGGGACG	AGTCCTGTTG	

FIGURE 14D
(SEQ ID NO. 10)

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3610	3620	3630	3640	3650	3660	3670	3680	3690
CCGGCCCTCC	TCTCACCAAGG	GTGCCCTCTGC	AGCCGCCACA	CACACACAGG	GGATCACACA	CCACGTCAAG	TCCCTGGCCC	TGGCCCACTT
GGTGGGAGG	AGAGTGTTC	CACGGGACG	TGGGGGTGT	GTTGTTGTTCC	CCTAGTGTGT	GGTGCACTGC	AGGGACGGG	ACCGGGTGA
3700	3710	3720	3730	3740	3750	3760	3770	3780
CCCAAGTCCG	CCCTTCCCTG	CAGGACGGAT	CAGCCCTCGAC	TGTGCCCTTCT	AGTTGCCAGC	CATCTGTTGT	TGCCCCCTCC	CCCGTGCCTT
GGGTCA CGGGC	GGGAAGGGAC	GTCCTGCCCTA	GTCGGAGCTG	ACACGGAAAGA	TCAACGGTGT	GTAGACAACA	AACGGGGAGG	GGGCACGGAA
3790	3800	3810	3820	3830	3840	3850	3860	3870
CCTTGACCCT	CGAAGGGGCC	ACTTCCCACTG	TCCTTTCCTA	ATTAATAATGAG	GAATAATGAG	CGCATTTGCT	GAGTAGGTGT	CATTCTATTG
GGAACTGGGA	CTTCCACGG	TGAGGGTGCAC	AGGAAAGGAT	TATTTTACTC	CTTTAACGTA	GCCTAACAGA	CTCATCACCA	GTAAAGATAAG
3880	3890	3900	3910	3920	3930	3940	3950	3960
TGGGGGTGG	GGTGGGAG	GACAGCAAGG	GGGAGGATTG	GGAGACAAT	AGCAGGGCATG	CTGGGGATGC	GGTGGGGTGT	ATGGCTTCTG
ACCCCCCACC	CCACCCCGTC	CTGTGTTCC	CCCTCCTAAC	CCTTCTGTAA	TGCTCCGTAC	GACCCCTACG	CCACCCGAGA	TACCGAAGAC
3970	3980	3990	4000	4010	4020	4030	4040	4050
AGGGGGAAAG	AACCAGCTGG	GGCTCTAGGG	GGTATCCCCA	CGGGCCCTGT	AGCGGGCGAT	TAAGGGGGGC	GGGGTGGGTG	GTTAACGGCA
TCCGCCCTTC	TGGTCGACC	CCGAGATCCC	CCATAGGGGT	GCGGGGGACA	TGCGCCGGTA	ATTGCGCCG	CCCACACCA	CAATGGCGGT
4060	4070	4080	4090	4100	4110	4120	4130	4140
CGGTGACCGC	TACACTGCC	AGGCCCTAG	CGCCCGCTCC	TTTGGCTTTC	TTCCTCTTCC	TTCCTGCCAC	GTTGCGGGGG	CCTCTCAAAA
CGCACTGGCG	ATGTGAACGG	TGCCGGGATC	GCGGGGAGG	AAAGCGAAAG	AAGGGAAAGGA	AAGAGGGGTG	CAAGGGCCCC	GGAGAGGTGTT
4150	4160	4170	4180	4190	4200	4210	4220	4230
AAGGGAAAAA	AAGGCATGCAT	CTCAATTAGT	CAGGAAACCAT	AGTCCCCCCC	CTAACTCCGC	CCATCTCCGC	CCTAACTCCG	CCCAAGTTCGG
TTCCCTTTTT	TTCGTTAGTA	GAGTTAATCA	GTGTTGTTGA	TCAAGGGGGG	GATTGAGGGG	GGTAGGGGGG	GGATTGAGGC	GGGTCAAAGGC
4240	4250	4260	4270	4280	4290	4300	4310	4320
CCCAATTCTCC	GGCCCATGGC	TGACTTAATT	TTTTTATTAA	TGCAAGGGGG	GAGGCCCT	GCGCTCTGAG	AAGTAGTGTG	TTCATCACTC
GGCTTAAGAGG	CGGGGGTACCG	ACTGTTAAA	AAAAATAATA	ACGTCTCCGG	CTCCGGGGGA	GCGGGAGACT	CGATAAGGTG	
4330	4340	4350	4360	4370	4380	4390	4400	4410
GAGGCTTTT	TGGAGGGCTA	GGCTTTTGCA	AAAAGCTTGG	ACAGCTCAAG	GCTGGGATTT	CGGGCCAAAC	TGACGGCAA	TCCTAGGGTG
CTCCGAAAAA	ACCTCCGGAT	CCGAAAACGT	TTTTCGAACG	TGTGAGTCC	CGACGCTAAA	GCGGGTTTG	AACTGCGGT	AGGATCGGCAC
4420	4430	4440	4450	4460	4470	4480	4490	4500
AAGGCTGGTA	GGATTGTTATC	CCCCCTGGCA	TCAATGGTTC	ACCATTTGAAAC	TGGATCGTCC	CCGTGCTTCC	AATATGGGG	ATTGGCAAG
TTCGGACCAT	CCTAAATAAG	GGGGCACGGT	AGTACCAAGC	TGGTAACCTG	ACGTAGGAGC	GGCACAGGGT	TTTATACCCC	TAACCCTTCT

FIGURE 14E
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4510	4520	4530	4540	4550	4560	4570	4580	4590
ACGGAGACCT	ACCCGGCCT	CCGGCTAGGA	ACGAGTCAA	GTACTCCAA	AGAATGCCA	CACCTCTTC	AGTGGAAAGGT	AAACAGAAC
TGCCCTCTGGA	GGGGACCGGA	GGCGAGTCCT	TGCTCAAGTT	CATGAAGGT	TCTTAAGGT	GTTGGAGAAG	TCACCTCCA	TTTGTCTTAG
4600	4610	4620	4630	4640	4650	4660	4670	4680
TGGTGATTAT	GGGTAGAAA	ACCTGGTTCT	CCATTCCCTGA	GAAGAATCGA	CCTTTAAGG	ACAGAATTAA	TATAGTCTC	AGTAGAGAAC
ACCACTAATA	CCCATCCCTT	TGGACCAAGA	GGTAAGGACT	CTTCTTAGCT	GGAAATTCTCC	TGTCTTAATT	ATATCAAGAG	TCATCTCTTG
4690	4700	4710	4720	4730	4740	4750	4760	4770
TCAAGAACC	ACCAAGGGA	GCTCATTTC	TGCCCCAAAAG	TTGGATGAT	GCCTTAAGAC	TTATTGAACA	ACCGGAATTG	GCAAGTAAG
AGTTTCTTGG	TGGTGGCTCT	CGAGTAAAAAG	AACGGTTTC	AAACCTACTA	CGGAATTCTG	AAATAACTGT	TGGCCCTTAAC	CGTTCATTTC
4780	4790	4800	4810	4820	4830	4840	4850	4860
TAGACATGGT	TTGGATAGTC	GGAGGCAGTT	CTGTTTACCA	GGAGGCCATG	AATCAACCAG	GCCACCTTAG	ACTCTTGTG	ACAAGGATCA
ATCTGTACCA	AACCTATCAG	CCTCCGTCAA	GACAAATGGT	CCTTCGGTAC	TTAGTGGTC	CGGTGGAATC	TGAGAAACAC	TGTTCCTTAGT
4870	4880	4890	4900	4910	4920	4930	4940	4950
TGCAGGAATT	TGAAAGTGCAC	ACGTTTTCC	CAGAAATGAA	TTTGGGAAA	TATAAACCTTC	TCCCAGAATA	CCCAGGGTC	CTCTCTGAGG
ACGTCCCTAA	ACTTTCAC TGCAAAAGG	GTCTTAACT	AAACCCCTTT	ATATTGAAG	AGGGCTTAT	GGGTCCGCAG	GAGAGACTCC	
4960	4970	4980	4990	5000	5010	5020	5030	5040
TCCAGGAGGA	AAAAGGCATC	AACTATAAGT	TTGAAGTCTA	CGAGAAAGAA	GACTAACAGG	AAGATGCTT	CAAGTCTCT	GCTCCCTCC
AGGTCCCTCT	TTTCCGTAG	TTCATATTCA	AACTTCAGAT	GCTCTTCTTT	CTGATTGTC	TTCTACGAAA	GTTCAGAGA	CGAGGGGAGG
5050	5060	5070	5080	5090	5100	5110	5120	5130
TAAGCTATG	CATTTTATA	AGACCATGGG	ACTTTTGTG	GCTTTAGTC	TCTTTGTGAA	GGAAACCTTAC	TTCCTGGGTG	TGACATAATT
ATTTGATAC	GTAAAAATAT	TCTGGTACCC	TGAAAAGCAC	CGAARCTAG	AGAAAACACTT	CCTTGGAAATG	AAGACACCAC	ACTCTATTAA
5140	5150	5160	5170	5180	5190	5200	5210	5220
GGACAAACTA	CCTACAGAGA	TTTAAAGCTC	TAAGGTAAT	ATAAAATTTC	TAAGTGTATA	ATGTGTAA	CTACTGATTC	TAATTGTTTG
CCTGTTGAT	GGATGTCCT	AAATTTCGAG	ATTCCATTAA	TATTTAAAAA	ATTACATAT	TACACATTT	GATGACTAAG	ATTAACAAAC
5230	5240	5250.	5260	5270	5280	5290	5300	5310
TGTATTTAG	ATTCCAACTT	ATGGAACCTGA	TGAATGGAG	CAGTGGTGG	ATGCCTTTAA	TGAGGAAAC	CTGTTTGCT	CAGAAGAAAT
ACATAAAATC	TAAGGTTGGA	TACCTTGACT	ACTTACCTC	GTCACCACT	TACGGAAATT	ACTCCTTTTG	GACAAACGA	GTCTTCTTTA
5320	5330	5340	5350	5360	5370	5380	5390	5400
GGCATCTAGT	GATGATGAGG	CTACTGCTGA	CTCTCAACAT	TCTACTCCTC	CAAAAAGAA	GAGAAAGCTA	AGGACCCCCA	AGGACTTTCC
CGGTAGATCA	CTACTACTCC	GATGACCGACT	GAGAGTGTGA	AGATGAGGAG	CTTCTTCTT	CTCTTCCAT	CTCTCTGGGT	TCC TGA AAGG

FIGURE 14F
(SEQ ID NO. 10)

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5410	5420	5430	5440	5450	5460	5470	5480	5490
TTCAGAATTG	CTAAGTTT	TGAGTCATGC	TGTGTTTAGT	ATAAGAACTC	TTGCTTGCTT	TGCTTATTAC	ACCACAAAGG	AAAAGCTGC
AAGTCTAAC	GATTCAAAA	ACTCAGTAAG	ACACAATCA	TTATCTTGA	AACGAACGA	ACGATAAATG	TGGTCTTCC	TTTTCGACG
5500	5510	5520	5530	5540	5550	5560	5570	5580
ACTGCTATAC	AAGAAATTAA	TGAAAAAATA	TTCTGTAACC	TTTATAAGTA	GGCATTAACAG	TTATAATCAT	AACATACTGT	TTTTTCTTAC
TGACGATATG	TTCTTTAAT	ACCTTTTAT	AGAACATTGG	AAATATTCAAT	CCGTATTGTC	ATATTTAGTA	TGTTATGACA	AAAAAGAAATG
5590	5600	5610	5620	5630	5640	5650	5660	5670
TCCACACAGG	CATAGGTGT	CTGCTTATAA	TAACATATGCT	CAAAAATTGT	GTACCTTTAG	CTTTTTAATT	TGTAAGGGG	TAAATAAGGA
AGGTGTGTC	GTATCTCAC	GACGATAATT	ATTGATACGA	GTTTTAACCA	CATGGAAATC	GAAAATTAA	ACATTCCCC	AATTATCCCT
5680	5690	5700	5710	5720	5730	5740	5750	5760
ATATTGATG	TATAGTGCC	TGACTAGAGA	TCATATACTAG	CCATACCACA	TTTGTAGAGG	TTTACTTGC	TTTAAAAAAC	CTCCCACACC
TATAAACTAC	ATATCACGGA	ACTGATCTCT	AGTATTAGTC	GGTATGGGT	ARACATCTCC	AAATGAAACG	AAATTTTTG	GAGGGTGTGG
5770	5780	5790	5800	5810	5820	5830	5840	5850
TCCCCCTGAA	CCTGAAACAT	AAAATGNAATG	CAATTGTTGT	TGTTAACTTG	TTTATGCGAG	CTTATAATGG	TTACAAATAA	AGCAATAGCA
AGGGGACTT	CGACTTGTAA	TTTACTTAC	GTAAACAAACA	ACAAATTGAAAC	ARATAACGTC	GAATATTAC	AATGTTTATT	TGTTATCGGT
5860	5870	5880	5890	5900	5910	5920	5930	5940
TCAAAATT	CAAAATAAA	GCATTTTTT	CACTGCAATT	TAGTTGTGGT	TTGTCAAAC	TCATCAATGT	ATCTTATCAT	GTCTGGATCG
AGTGTAA	GTGTTTATT	CGTAAAAA	GTGACGTTAAG	ATCAACACCA	AAACAGTTTG	AGTAGTTACA	TAGAATAGTA	CAGACCTAGC
5950	5960	5970	5980	5990	6000	6010	6020	6030
GCTGGATGAT	CCTCCAGGCC	GGGGATCTCA	TGCTGGAGTT	CCTCGCCAC	CCCAAACCTGT	TTATTGCAAGC	TTTATAATGGT	TACAAATAAA
CGACCTACTA	GGAGGTCGG	CCCCTAGAGT	ACGACCTCAA	GAAGGGGGTG	GGGTGAACA	ATAAACGTCG	AAATATACCA	ATGTTTATTT
6040	6050	6060	6070	6080	6090	6100	6110	6120
GCATAAGCAT	CACAAATTTC	ACAAATTAAG	CATTTTTC	ACTGCCATTCT	AGTTGTGGTT	TGTCCAACACT	CATCAATGTA	TCTTATCATG
CGTTATCGTA	GTGTTAAG	TGTTTATTTC	GTAAAAAAG	TGACGTAAGA	TCAACACCA	ACAGGTTGGA	GTAGTTACAT	AGAATAGTAC
6130	6140	6150	6160	6170	6180	6190	6200	6210
TCTGTATAC	GTGGAACCTCT	AGCTAGAGCT	TGCGGTAAATC	ATGGTCATAG	CTGTTCCCTG	TGTGAATTG	TTATCGCCTC	ACAATTCCAC
AGACATATGG	CAGCTGGAGA	TGATCTCGA	ACCGGATTAG	TACCAAGTATC	GACAAAGGAC	ACACTTAAAC	AATAGGGAG	TGTTAAAGGTG
6220	6230	6240	6250	6260	6270	6280	6290	6300
ACAAACATAG	AGCCGGAAAGC	ATAAAAGTGTAA	AAGCCCTGGGG	TGCCTTAATGA	GTGAGCTAAC	TCACATTAAAT	TGCGTGTGCGC	TCACTGGCCCG
TGTTGTATGC	TGGGCCATCG	TATTTCACAT	TTCGGGACCCC	ACGGATTACT	CACTCGATTG	AGTGTAATTA	ACGCAACGGG	AGTGACGGG

FIGURE 14G
(SEQ ID NO. 10)

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6310	6320	6330	6340	6350	6360	6370	6380	6390
CCTTCCAGTC	GGGAAACCTG	TGTTGCCAGC	TGCATTAAATG	AATCGGCCAA	CGCGGGGA	GAGGGGGT	GGCTATGGG	CCCTCTTCGG
GAAGGTCA	CCCTTGAC	ACGACGGTCC	ACGTAATTAC	TTAGCCGGT	GGCGCCCC	CTCCGCCAA	GGCATTAACCC	GGAGAAAGGC
6400	6410	6420	6430	6440	6450	6460	6470	6480
CTTCCTCGT	CACTGACTCG	TGTTCCGGT	GGGGCGAGGC	GTATCAGTC	ACTCAAAGGC	GGTAATAACGG	TTATCCACAG	
GAAGGGCGA	GTGACTGAGC	AGCGGAGCC	AGCAAGCCG	GGCGCTCGC	CATAGTCGAG	TGAGTTCCG	CCATTATGCC	ATAGGTGTC
6490	6500	6510	6520	6530	6540	6550	6560	6570
AATCAGGGG	TAACGGAGGA	AAGAACATGT	GAGCAAAAGG	CCAGCAAAAG	GGCAGGAACC	GTAAAAAGGC	CCGGTGTGCTG	GCGRGTTTC
TTAGTCCCCT	ATTCGGTCCCT	TTCTTGTACA	CTCGTTTCC	GGTCGTTTCC	GGTCCTTGG	CATTTTTCCG	GCGCACGAC	CGCAAAAGG
6580	6590	6600	6610	6620	6630	6640	6650	6660
ATAGGCTCCG	CCCCCTGAC	GAGCATCAC	AAAATCGACG	CTCAAGTCAG	AGGTGGCGAA	ACCCGACAGG	ACTATAAAGA	TACCAAGGGT
TATCCGAGGC	GGGGGACTG	CTCGTAGTTGT	TTTGTGCTG	GAGTCAGTC	TCCACCGCTT	TGGGCTGTTC	TGATTTTCT	ATGGTCCGCA
6670	6680	6690	6700	6710	6720	6730	6740	6750
TTCCCCCTGG	AAAGCTCCCTC	GTGCGCTCTC	CTGTTCCGAC	CCTGGCCGTT	ACCGGATACC	TGTCCGCCCT	TCTCCCTTCG	GAAGGGTGG
AGGGGGGAC	TTTGGGGAG	CAAGGGAG	GACAAGGGTG	GGACGGGAA	TGGCCATAGG	ACAGGGGGAA	AGAGGGAAAGC	CCTTCGCAC
6760	6770	6780	6790	6800	6810	6820	6830	6840
CGCTTCTCA	ATGCTACGC	TGTTAGGTATC	TCAGTTGGT	GTAGGTGCTT	CGCTCCAAGC	TGGGCTGTGT	GCACGAAACC	CCCGTTCAAC
GGAAAAGAGT	TACGAGTGGC	ACATCCATAG	AGTCAGGCCA	CATCCAGCAA	GCGAGGTTTG	ACCCGACACA	CYTGTCTGG	GGGCAAGTCG
6850	6860	6870	6880	6890	6900	6910	6920	6930
CCGACCGCTG	CGCTTATCC	GGTAACTATC	GTCTTAGTC	CAACCCGGTA	AGACACGACT	TATGCCACT	GGCAGCAGCC	ACTGGTAACA
GGCTGGCGAC	GGGAATAGG	CCATTGATAG	CAGAACTCAG	GTGGGCCAT	TCTGTGCTGA	ATAGGGTGA	CCGTGTCTGG	TGACCATTTG
6940	6950	6960	6970	6980	6990	7000	7010	7020
GGATTAGCAG	AGCGAGGTAT	GTAGGGGGTG	CTACAGAGTT	CTTGAAGTGG	TGGCCCTAAC	ACGGCTACAC	TAGAAGGACA	GTATTGGTA
CTTAATCGTC	TCGCTCATA	CATCCGCCAC	GATGTCCTAA	GAACCTCAC	ACGGGATTGA	TGCGATGTG	ATCTTCTGT	CATRAACCAT
7030	7040	7050	7060	7070	7080	7090	7100	7110
TCTGGGCTC	GCTGAAAGCCA	GTACCTTCG	GAAAAGAGT	TGATCAGCTT	TGATCAGCT	ACAAACCAC	CGCTGTAGC	GCTGGTTTT
AGACGCCAGA	CGACTTCGGT	CAATCGAAC	CTTTTCTCA	ACCATCGAGA	ACTAGGCCGT	TGTTTGGTG	GCGACCATCG	CCACCAAA
7120	7130	7140	7150	7160	7170	7180	7190	7200
TGTTTGCA	GCAGGAGT	ACGGCGAGA	AAAAAGGATC	TCAAGAAGAT	CCCTTGATCT	TTCTACGGG	GTCTGACGCT	CAGTGGAACG
ACAAACGTT	CGTCGTCTAA	TGCGGTCTT	TTTTTCTAG	AGTCTCTCTA	GGAAACTAGA	AAAGATGCC	CAGAFTGCGA	GTCACCTTCG

FIGURE 14H
(SEQ ID NO. 10)

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7210	7220	7230	7240	7250	7260	7270	7280	7290
AAAACCTACG	TAAAGGGATT	TTGGTCATGA	GATTCAAA	AAGGATCTTC	ACCTAGATCC	TTTTAAATTAA	AAAATGAAGT	TTAAATCAGA
TTTTGAGTGC	AATMCCCTAA	AACCGACTACT	CTAATAGTTT	TTCCCTAGAA	TGGATCTAGG	AAAATTAAAT	TTTTACTTC	AAATTTAGT
7300	7310	7320	7330	7340	7350	7360	7370	7380
TCTAAAGTAT	ATATGAGTAA	ACTTGGTCTG	ACAGTTACCA	ATGCTTAATC	AGTGAAGGCAC	CTATCTCAGC	GATCTGTCTA	TTTCGTTCAT
AGATTTCAT	TATACTCATT	TGAACCAGAC	TGTCAATTGCT	TACGAATTAG	TCACTCGTG	GATAGAGTGC	CTAGACAGAT	AAAGCAAGTA
7390	7400	7410	7420	7430	7440	7450	7460	7470
CCATAGTTGC	CTGACTCCCC	GTGGTGTAGA	TAACTACGAT	ACGGAGGGC	TTACCCATCTG	GCCCCAGTGC	TGCCATGTATA	CCGGGAGAC
GGTATCAACG	GACTGAGGGG	CAGCACATCT	ATTGATGCTA	TGCCCCTCCCG	AATGGTAGAC	GGGGTCAGC	ACGTTACTAT	GGGCTCTGG
7480	7490	7500	7510	7520	7530	7540	7550	7560
CACGGCTCACC	GGCTCCAGAT	TTATCAGCAA	TAACCAAGCC	AGCCGGAAAGG	GCCGAGCGCA	GAAGTGGTC	TGCAAACTTTA	TCGGCCTCCA
GTGGCAGTGG	CCGAGGTCTA	AATAGTCGT	ATTGGTCGG	TCGGCCCTTC	CGGCTCGGT	CTTCACCAAG	ACGTTGAAAT	AGGGGAGGT
7570	7580	7590	7600	7610	7620	7630	7640	7650
TCCAGTCTAT	TAATTGTTGC	CGGGGAAGCTA	GAGTAAGTAG	TTGGCCAGT	AATAGTTTGC	GAAACGTTGT	TGCCATTGCT	ACAGGCATCG
AGGTCAAGATA	ATTAACAAACG	GCCCTTCGAT	CTCATTCATC	AAGGGTCAA	TTATCAAACG	CGTTGCAACA	ACGGTTRACGA	TGTCCTGTAGC
7660	7670	7680	7690	7700	7710	7720	7730	7740
TGGGTGTACG	CTCGTCGTT	GGTATGGCTT	CATTCACTC	CGGTTCCTAA	CGATCAAGGC	GAGTTACATG	ATCCCCCATG	TGGTCARAA
ACACAGTGC	GAGCAGRAA	CCATACCGAA	GTAAGTCGAG	GCCAAGGGTT	GCTAGTTCCG	CTCAATGTAC	TAGGGGTAC	ACACAGTTT
7750	7760	7770	7780	7790	7800	7810	7820	7830
AAGCGGGTTAG	CTCCCTTGGGT	CCTCCGATCG	TTGTCAAGAAG	TAAGTTGGCC	GCAGTGTAT	CACTCATGGT	TATGGCAGCA	CTGCTATAAT
TTCGCCAATC	GAGGAAGCCA	GGAGGCTAGC	AACAGCTTC	ATTCAACCGG	CGTCACAAATA	GTGAGTACCA	ATACCGTGT	GACGTATTA
7840	7850	7860	7870	7880	7890	7900	7910	7920
CTCTTACTGT	CATGCCATCC	GTAAAGATGCT	TTTCTGTGAC	TGGTGAATAC	TCAACCAAGT	CATTCTGAGA	ATAGTGTATG	CCGGACCGA
GAGAATGACA	GTACGGTAGG	CATTCTACGA	AAAGACACTG	ACCACTCATG	AGTTGGTTCA	GTAAAGACTCT	TATCACATAC	GGCGCTGGGT
7930	7940	7950	7960	7970	7980	7990	8000	8010
GTGGCTCTG	CCGGGGCTCA	ATACGGGATA	ATACCGGCC	ACATAGCAGA	ACTTTAAAG	TGCTCATCAT	TCGAAAAACGT	TCTTCGGGGC
CAACGAGAAC	GGGGCGCAGT	TATGCCCTAT	TATGGCCCG	TGTATCGTCT	TGAATTTTC	ACGAGTAGTA	ACCTTTGCA	AGAAGCCCCG
8020	8030	8040	8050	8060	8070	8080	8090	8100
GAATAACTCTC	AAGGATCTTA	CCGGCTGTTGA	GATCCAGTTC	ACTCGTAACCC	CCAACTGATC	TTCAGGATCT	TTTACTTTCA	
CTTTGAGAG	TTCCCTAGAAT	GGCCGACAAT	CTACATTGGG	GGAGGACGTG	GGAGGACGTG	AAGTGTAGA	AAAGTGTAGA	AAATGAAAGT

FIGURE 14I
(SEQ ID NO. 10)

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8110	TGGGTGAGCA	AAACAGGAA	8130	GGCAAAATGC	CGCAAAAAAG	8140	GGAATAAGGG	CGAACACGGG	8150	CGACACGGAA	ATGTTGAATA	8160	CTCATACTCT	8170	ATGTTGAATA	CTCATACTCT	8180	8190
	GGTCGAAAG	ACCCACTCGT	TTTGTGTCCTT	CCGTTTACG	GGGTTTTTC	CCTTATTCCC	GCTGTGCCRT	TACAACCTAT	GAGTATGAGA									
8200	TCCTTTTCA	ATATTATGA	AGCATTATC	8220	AGGGTTATTG	TCTCATGAGC	8230	8240	8250	8260	8270	8280						
	AGGAAAAGT	TATAATACT	TCTGTTAAATAG		TCCCCAATAAC	GGATACATAT	TTGAAATGTAT											
8290	GGGTTCCGGG	CACATTCCC	CGAAAAGTGC	8300	8310	8320	8330											
	CCGAAAGGGC	GTGTAAGGGG	GCTTTTCACG					CACCTGACGT	C									
								GTGGGACTGCA	G									

FIGURE 14J
SEQ ID NO. 10)



FIGURE 18A (SEQ ID NO. 22)

1 GGTACCAATT TAAATTGATA TCTCCTTAGG TCTCGAGTCT CTAGATAACC
51 GGTCAATCGA TTGGAATTCT TGCGGCCGCT TGCTAGCCAC CATGGAGTTG
101 TGGTTAACGCT TGGTCTTCCT TGTCCTTGTT TTAAAAGGTG TCCAGTGTGA
151 AGTGCAACTG GTGGAGTCTG GGGGAGGCTT AGTGCAGCCT GGAGGGTCCC
201 TGCGACTTTC CTGTGCTGCA TCTGGATTCC CGTTCAGTGA CTATTACATG
251 TATTGGGTTTC GCCAGGCTCC AGGCAAGGGA CTGGAGTGGG TCTCATACAT
301 TAGTCAAGAT GGTGATATAA CCGACTATGC AGACTCCGTA AAGGGTCGAT
351 TCACCATCTC CAGAGACAAT GCAAAGAACCA GCCTGTACCT GCAAATGAAC
401 AGCCTGAGGG ACGAGGACAC AGCCGTGTAT TACTGTGCAA GAGGCCTGGC
451 GGACGGGGCC TGGTTTGCTT ACTGGGGCCA AGGGACTCTG GTCACGGTCT
501 CTTCCGCTAG CACCAAGGGC CCATCGGTCT TCCCCCTGGC ACCCTCCTCC
551 AAGAGCACCT CTGGGGGCAC AGCGGCCCTG GGCTGCCTGG TCAAGGACTA
601 CTTCCCCGAA CCGGTGACGG TGTCGTGGAA CTCAGGCGCC CTGACCAGCG
651 GCGTGCACAC CTTCCCGGCT GTCCTACAGT CCTCAGGACT CTACTCCCTC
701 AGCAGCGTGG TCACCGTGCC CTCCAGCAGC TTGGGCACCC AGACCTACAT
751 CTGCAACGTG AATCACAAGC CCAGCAACAC CAAGGTGGAC AAGAAAGTTG
801 GTGAGAGGCC AGCACAGGGA GGGAGGGTGT CTGCTGGAAG CCAGGCTCAG
851 CGCTCCTGCC TGGACGCATC CCGGCTATGC AGCCCCAGTC CAGGGCAGCA
901 AGGCAGGCC CGTCTGCCTC TTCACCCGGA GGCTCTGCC CGCCCCACTC
951 ATGCTCAGGG AGAGGGTCTT CTGGCTTTT CCCCAGGCTC TGGGCAGGCA
1001 CAGGCTAGGT GCCCTAAACC CAGGCCCTGC ACACAAAGGG GCAGGTGCTG
1051 GGCTCAGACC TGCCAAGAGC CATATCCGGG AGGACCCCTGC CCCTGACCTA
1101 AGCCCACCCC AAAGGCCAAA CTCTCCACTC CCTCAGCTCG GACACCTTCT
1151 CTCCTCCCAG ATTCCAGTAA CTCCCAATCT TCTCTCTGCA GAGCCAAAT
1201 CTTGTGACAA AACTCACACA TGCCCACCGT GCCCAGGTAA GCCAGCCCAG
1251 GCCTCGCCCT CCAGCTCAAG GCAGGACAGG TGCCCTAGAG TAGCCTGCAT
1301 CCAGGGACAG GCCCCAGCCG GGTGCTGACA CGTCCACCTC CATCTCTTCC

235 237

1351 TCAGCACCTG AACTCTGG GGGACCGTCA GTCTTCCTCT TCCCCCAA
1401 ACCCAAGGAC ACCCTCATGA TCTCCCGGAC CCCTGAGGTC ACATGCGTGG
1451 TGGTGGACGT GAGCCACGAA GACCCTGAGG TCAAGTTCAA CTGGTACGTG
1501 GACGGCGTGG AGGTGCATAA TGCCAAGACA AAGCCGCGGG AGGAGCAGTA
1551 CAACAGCACG TACCGTGTGG TCAGCGTCCT CACCGTCCTG CACCAGGACT
1601 GGCTGAATGG CAAGGATTAC AAGTGCAAGG TCTCCAACAA AGCCCTCCC
1651 GCCCCATCG AGAAAACCAT CTCCAAAGCC AAAGGTGGGA CCCGTGGGT
1701 GCGAGGGCCA CATGGACAGA GGCCGGCTCG GCCCACCCCTC TGCCCTGAGA
1751 GTGACCGCTG TACCAACCTC TGTCCCTACA GGGCAGCCCC GAGAACACAA
1801 GGTGTACACC CTGCCCAT CCCGGATGA GCTGACCAAG AACCAAGTCA
1851 GCCTGACCTG CCTGGTCAAA GGCTTCTATC CCAGCGACAT CGCCGTGGAG
1901 TGGGAGAGCA ATGGGCAGCC GGAGAACAAAC TACAAGACCA CGCCTCCGT
1951 GCTGGACTCC GACGGCTCCT TCTTCCTCTA CAGCAAGCTC ACCGTGGACA
2001 AGAGCAGGTG GCAGCAGGGG AACGTCTTCT CATGCTCCGT GATGCATGAG
2051 GCTCTGCACA ACCACTACAC GCAGAAGAGC CTCTCCCTGT CTCCGGTAA
2101 ATGAGTGCAG CCGCCGGCAA GCCCCGCTC CCCGGCTCT CGCGGTGCA
2151 CGAGGATGCT TGGCACGTAC CCCCTGTACA TACTTCCCGG GCGCCCAGCA
2201 TGGAAATAAA GCACCCAGCG CTGCCCTGGG CCCCTGCGAG ACTGTGATGG
2251 TTCTTCCAC GGGTCAGGCC GAGTCTGAGG CCTGAGTGGC ATGAGGGAGG
2301 CAGAGCGGGT CCCACTGTCC CCACACTGGC CCAGGCTGTG CAGGTGTGCC
2351 TGGGCCCCCT AGGGTGGGGC TCAGCCAGGG GCTGCCCTCG GCAGGGTGGG
2401 GGATTGCCA GCGTGGCCCT CCCTCCAGCA GCACCTGCC TGGGCTGGGC
2451 CACGGGAAGC CCTAGGAGCC CCTGGGGACA GACACACAGC CCCTGCCTCT
2501 GTAGGAGACT GTCCTGTTCT GTGAGGCC CCCTGCCTCC GACCTCCATG
2551 CCCACTCGGG GGCATGCCTA GTCCATGTGC GTAGGGACAG GCCCTCCCTC
2601 ACCCATCTAC CCCCCACGGCA CTAACCCCTG GCTGCCCTGC CCAGCCTCGC
2651 ACCCGCATGG GGACACAAACC GACTCCGGGG ACATGCACTC TCGGGCCCTG
2701 TGGAGGGACT GGTGCAGATG CCCACACACA CACTCAGCCC AGACCCGTT
2751 AACAAACCCC GCACTGAGGT TGGCCGGCCA CACGGCCACC ACACACACAC
2801 GTGCACGCCT CACACACGGA GCCTCACCCG GGCGAACTGC ACAGCACCCA

FIGURE 18B (SEQ ID NO. 22)

2851 GACCAGAGCA AGGTCTCGC ACACGTGAAC ACTCCTCGGA CACAGGCC
2901 CACGAGCCCC ACGCGGCACC TCAAGGCCA CGAGCCTCTC GGCAGCTTCT
2951 CCACATGCTG ACCTGCTCAG ACAAAACCCAG CCCTCCTCTC ACAAGGGTGC
3001 CCCTGCAGCC GCCACACACA CACAGGGGAT CACACACCAC GTCACGTCCC
3051 TGGCCCTGGC CCACTTCCA GTGCCGCCCT TCCCTGCAGG ACGGATCAGC
3101 CTCGACTGTG CCTTCTAGTT GCCAGCCATC TGTTGTTGC CCCTCCCCG
3151 TGCCTTCCTT GACCCTGGAA GGTGCCACTC CCACTGTCTT TTCCCTAATAA
3201 AATGAGGAAA TTGCATCGCA TTGTCTGAGT AGGTGTCATT CTATTCTGGG
3251 GGGTGGGGTG GGGCAGGACA GCAAGGGGGA GGATTGGAA GACAATAGCA
3301 GGCATGCTGG GGATGCCGTG GGCTCTATGG CTTCTGAGGC GGAAAGAAC
3351 AGCTGGGCT CTAGGGGTA TCCCCACGCG CCCTGTAGCG GCGCATTAAG
3401 CGCGGCCGGT GTGGTGGTTA CGCGCAGCGT GACCGCTACA CTTGCCAGCG
3451 CCCTAGCGCC CGCTCCTTTC GCTTCTTCC CTTCTTTCT CGCCACGTTC
3501 GCCGGGCCTC TCAAAAAAAGG GAAAAAAAGC ATGCATCTCA ATTAGTCAGC
3551 AACCATAGTC CCGCCCCCAA CTCCGCCCAT CCCGCCCTA ACTCCGCCA
3601 GTTCCGCCCA TTCTCCGCC CATGGCTGAC TAATTTTTT TATTATGCA
3651 GAGGCCGAGG CCGCCTCGGC CTCTGAGCTA TTCCAGAAGT AGTGAGGAGG
3701 CTTTTTGGA GCCCTAGGCT TTTGAAAAA GCTTGGACAG CTCAGGGCTG
3751 CGATTCGCG CCAAACCTGA CGGCAATCCT AGCGTGAAGG CTGGTAGGAT
3801 TTTATCCCCG CTGCCATCAT GGTCGACCA TTGAAC TGCA TCGTCGCCGT
3851 GTCCCCAAAT ATGGGGATTG GCAAGAACGG AGACCTACCC TGGCCTCCGC
3901 TCAGGAACGA GTTCAAGTAC TTCCAAAGAA TGACCACAAAC CTCTCAGTG
3951 GAAGGTAAAC AGAATCTGGT GATTATGGGT AGGAAAACCT GGTTCTCCAT
4001 TCCTGAGAAG AATCGACCTT TAAAGGACAG AATTAATATA GTTCTCAGTA
4051 GAGAACTCAA AGAACCAACCA CGAGGAGCTC ATTTCTTGC CAAAAGTTG
4101 GATGATGCCT TAAGACTTAT TGAACAACCG GAATTGGCAA GTAAAGTAGA
4151 CATGGTTTGG ATAGTCGGAG GCAGTTCTGT TTACCAGGAA GCCATGAATC
4201 AACCAAGGCCA CCTTAGACTC TTTGTGACAA GGATCATGCA GGAATTGAA
4251 AGTGACACGT TTTTCCCAGA AATTGATTG GGGAAATATA AACTTCTCCC
4301 AGAATACCCA GGCGTCCTCT CTGAGGTCCA GGAGGAAAAA GGCATCAAGT

FIGURE 18C (SEQ ID NO. 22)

4351 ATAAGTTGA AGTCTACGAG AAGAAAGACT AACAGGAAGA TGCTTCAG
4401 TTCTCTGCTC CCCTCCTAAA GCTATGCATT TTTATAAGAC CATGGGACTT
4451 TTGCTGGCTT TAGATCTCTT TGTGAAGGAA CCTTACTTCT GTGGTGTGAC
4501 ATAATTGGAC AAACTACCTA CAGAGATTAA AAGCTCTAAG GTAAATATAA
4551 AATTTTAAG TGTATAATGT GTTAAACTAC TGATTCTAAT TGTTGTGTA
4601 TTTTAGATTC CAACCTATGG AACTGATGAA TGGGAGCAGT GGTGGAATGC
4651 CTTTAATGAG GAAAACCTGT TTTGCTCAGA AGAAATGCCA TCTAGTGATG
4701 ATGAGGCTAC TGCTGACTCT CAACATTCTA CTCCTCCAAA AAAGAAGAGA
4751 AAGGTAGAAG ACCCCAAGGA CTTTCCTTCA GAATTGCTAA GTTTTGAG
4801 TCATGCTGTG TTTAGTAATA GAACTCTTGC TTGCTTGCT ATTTACACCA
4851 CAAAGGAAAA AGCTGCACTG CTATACAAGA AAATTATGGA AAAATATTCT
4901 GTAACCTTTA TAAGTAGGCA TAACAGTTAT AATCATAACA TACTGTTTT
4951 TCTTACTCCA CACAGGCATA GAGTGTCTGC TATTAATAAC TATGCTCAA
5001 AATTGTGTAC CTTAGCTTT TTAATTGTA AAGGGGTTAA TAAGGAATAT
5051 TTGATGTATA GTGCCTTGAC TAGAGATCAT AATCAGCCAT ACCACATTTG
5101 TAGAGGTTTT ACTTGCTTTA AAAAACCTCC CACACCTCCC CCTGAACCTG
5151 AACATAAAAA TGAATGCAAT TGTTGTTGTT AACTTGTTA TTGCAGCTTA
5201 TAATGGTTAC AAATAAAGCA ATAGCATCAC AAATTCACA AATAAAGCAT
5251 TTTTTCACT GCATTCTAGT TGTGGTTGT CCAAACATCAT CAATGTATCT
5301 TATCATGTCT GGATCGGCTG GATGATCCTC CAGCGCGGGG ATCTCATGCT
5351 GGAGTTCTTC GCCCACCCCA ACTTGTTTAT TGAGCTTAT AATGGTTACA
5401 AATAAAGCAA TAGCATCACA AATTCACAA ATAAAGCATT TTTTCACTG
5451 CATTCTAGTT GTGGTTTGTC CAAACATC AATGTATCTT ATCATGTCTG
5501 TATACCGTCG ACCTCTAGCT AGAGCTTGGC GTAATCATGG TCATAGCTGT
5551 TTCCTGTGTG AAATTGTTAT CCGCTCACAA TTCCACACAA CATACTGCC
5601 GGAAGCATAA AGTGTAAAGC CTGGGGTGCC TAATGAGTGA GCTAACTCAC
5651 ATTAATTGCG TTGCGCTCAC TGCCCCCTT CCAGTCGGGA AACCTGTCGT
5701 GCCAGCTGCA TTAATGAATC GGCCAACGCG CGGGGAGAGG CGGTTGCGT
5751 ATTGGGCGCT CTTCCGCTTC CTCGCTCACT GACTCGCTGC GCTCGGTCGT
5801 TCGGCTGCGG CGAGCGGTAT CAGCTCACTC AAAGGCGGTA ATACGGTTAT

FIGURE 18D (SEQ ID NO. 22)

5851 CCACAGAATC AGGGATAAC GCAGGAAAGA ACATGTGAGC AAAAGGCCAG
5901 CAAAAGGCCA GGAACCGTAA AAAGGCCGCG TTGCTGGCGT TTTTCCATAG
5951 GCTCCGCCCC CCTGACGAGC ATCACAAAAA TCGACGCTCA AGTCAGAGGT
6001 GGCGAAACCC GACAGGACTA TAAAGATACC AGGCCTTCC CCCTGGAAGC
6051 TCCCTCGTGC GCTCTCCTGT TCCGACCCCTG CCGCTTACCG GATACCTGTC
6101 CGCCTTCCTC CCTTCGGGAA GCGTGGCGCT TTCTCAATGC TCACGCTGTA
6151 GGTATCTCAG TTCGGTGTAG GTCGTTCGCT CCAAGCTGGG CTGTGTGCAC
6201 GAACCCCCCG TTCAGCCCCA CCGCTGCGCC TTATCCGGTA ACTATCGTCT
6251 TGAGTCCAAC CCGGTAAGAC ACGACTTATC GCCACTGGCA GCAGCCACTG
6301 GTAACAGGAT TAGCAGAGCG AGGTATGTAG GCGGTGCTAC AGAGTTCTTG
6351 AAGTGGTGGC CTAACTACGG CTACACTAGA AGGACAGTAT TTGGTATCTG
6401 CGCTCTGCTG AAGCCAGTTA CCTTCGGAAA AAGAGTTGGT AGCTCTTGAT
6451 CCGGCAAACA AACCAACCGCT GGTAGCGGTG GTTTTTTGT TTGCAAGCAG
6501 CAGATTACGC GCAGAAAAAA AGGATCTCAA GAAGATCCTT TGATCTTTTC
6551 TACGGGGTCT GACGCTCAGT GGAACGAAAA CTCACGTTAA GGGATTTGG
6601 TCATGAGATT ATCAAAAAGG ATCTTCACCT AGATCCTTT AAATTAAAAA
6651 TGAAGTTTA AATCAATCTA AAGTATATAT GAGTAAACTT GGTCTGACAG
6701 TTACCAATGC TTAATCAGTG AGGCACCTAT CTCAGCGATC TGTCTATTTC
6751 GTTCATCCAT AGTGCCTGA CTCCCCGTG TGAGATAAAC TACGATAACGG
6801 GAGGGCTTAC CATCTGGCCC CAGTGCTGCA ATGATAACCGC GAGACCCACG
6851 CTCACCGGCT CCAGATTTAT CAGCAATAAA CCAGCCAGCC GGAAGGGCCG
6901 AGCGCAGAAG TGGCCTGCA ACTTTATCCG CCTCCATCCA GTCTATTAAT
6951 TGTTGCCGGG AAGCTAGAGT AAGTAGTTCC CCAGTTAATA GTTGCGCAA
7001 CGTTGTTGCC ATTGCTACAG GCATCGTGGT GTCACGCTCG TCGTTGGTA
7051 TGGCTTCATT CAGCTCCGGT TCCCAACGAT CAAGGCGAGT TACATGATCC
7101 CCCATGTTGT GCAAAAAAGC GGTTAGCTCC TTGGTCCCTC CGATCGTTGT
7151 CAGAAGTAAG TTGGCCGCAG TGTTATCACT CATGGTTATG GCAGCACTGC
7201 ATAATTCTCT TACTGTCATG CCATCCGTAA GATGCTTTTC TGTGACTGGT
7251 GAGTACTCAA CCAAGTCATT CTGAGAATAG TGTATGCGGC GACCGAGTTG
7301 CTCTTGCCCCG GCGTCAATAC GGGATAATAC CGCGCCACAT AGCAGAACTT

FIGURE 18E (SEQ ID NO. 22)

7351 TAAAAGTGC CATCATTGGA AAACGTTCTT CGGGCGAAA ACTCTCAAGG
7401 ATCTTACCGC TGTTGAGATC CAGTCGATG TAACCCACTC GTGCACCCAA
7451 CTGATCTTCA GCATCTTTA CTTTCACCAG CGTTTCTGGG TGAGCAAAAA
7501 CAGGAAGGCA AAATGCCGCA AAAAAGGGAA TAAGGGCGAC ACGGAAATGT
7551 TGAATACTCA TACTCTTCCT TTTCAATAT TATTGAAGCA TTTATCAGGG
7601 TTATTGTCTC ATGAGCGGAT ACATATTGA ATGTATTTAG AAAAATAAAC
7651 AAATAGGGGT TCCGCGCACA TTTCCCCGAA AAGTGCCACC TGACGTCGAC
7701 GGATCGGGAG ATCTGCTAGG TGACCTGAGG CGCGCCGGCT TCGAATAGCC
7751 AGAGTAACCT TTTTTTTAA TTTTATTTA TTTTATTTT GAGATGGAGT
7801 TTGGCGCCGA TCTCCCGATC CCCTATGGTC GACTCTCAGT ACAATCTGCT
7851 CTGATGCCGC ATAGTTAACG CAGTATCTGC TCCCTGCTTG TGTGTTGGAG
7901 GTCGCTGAGT AGTGCAGGAG CAAAATTAA GCTACAACAA GGCAAGGCTT
7951 GACCGACAAT TGCATGAAGA ATCTGCTTAG GGTTAGGCGT TTTGCGCTGC
8001 TTCGCGATGT ACGGGCCAGA TATA CGCTT GACATTGATT ATTGACTAGT
8051 TATTAATAGT AATCAATTAC GGGTCATTA GTTCATAGCC CATATATGGA
8101 GTTCCCGCGTT ACATAACTTA CGGTAAATGG CCCGCCTGGC TGACCGCCCA
8151 ACGACCCCCG CCCATTGACG TCAATAATGA CGTATGTTCC CATAGTAACG
8201 CCAATAGGGA CTTTCCATTG ACGTCAATGG GTGGACTATT TACGGTAAAC
8251 TGCCCAC TTGACGTCAA TGACGGTAAA TGGCCCGCCT GGCATTATGC CCAGTACATG
8301 TTGACGTCAA TGACGGTAAA TGGCCCGCCT GGCATTATGC CCAGTACATG
8351 ACCTTATGGG ACTTTCTAC TTGGCAGTAC ATCTACGTAT TAGTCATCGC
8401 TATTACCATG GTGATGCGGT TTTGGCAGTA CATCAATGGG CGTGGATAGC
8451 GGTTTGACTC ACGGGGATT CCAAGTCTCC ACCCATTGA CGTCAATGGG
8501 AGTTTGTGTTT GGCACCAAAA TCAACGGGAC TTTCCAAAT GTCGTAACAA
8551 CTCCGCCCA TTGACGCAA TGCGGTAG GCGTGTACGG TGGGAGGTCT
8601 ATATAAGCAG AGCTCTCTGG CTAACTAGAG AACCCACTGC TTACTGGCTT
8651 ATCGAAATTA ATACGACTCA CTATAGGGAG ACCCAAGCTT

FIGURE 18F (SEQ ID NO. 22)

FIGURE 19 A
(SEQ ID NO. 23)

pD17-hG1b

10 20 30 40 50 60
GGTACCAATT TAAATTGATA TCTCCTTAGG TCTCGAGTCT CTAGATAACC GGTCAATCGA
CCATGGTTAA ATTAACTAT AGAGGAATCC AGAGCTCAGA GATCTATTGG CCAGTTAGCT

70 80 90 100 110 120
TGGAAATTCT TGCGGCCGCT TGCTAGCACC AAGGGCCCAT CGGTCTTCCC CCTGGCACCC
AACCTTAAGA ACGCCGGCGA ACGATCGTGG T'CCCCGGTA GCCAGAAGGG GGACCGTGGG

130 140 150 160 170 180
TCCTCCAAGA GCACCTCTGG GGGCACAGCG GCCCTGGGCT GCCTGGTCAA GGACTACTTC
AGGAGGT'TCT CG'GGGAGACC CCCGTGTCGC CGGGACCCGA CGGACCAGTT CCTGATGAAG

190 200 210 220 230 240
CCCGAACCGG TGACGGGTGTC GTGGAAACTCA GGCGCCCTGA CCAGGGGGGT GCACACCTTC
GGGCTTGGCC ACTGCCACAG CACCTTGAGT CGGGGGACT GGTGCCGCA CGTGTGGAAAG

250 260 270 280 290 300
CCGGC'GTCC TACAGTCCTC AGGACTCTAC TCCCCTCAGCA GCGTGGTCA CG'GGCCCTCC
GGCCGACAGG ATGTCAGGAG TCCTGAGATG AGGGAGTCGT CGCACCAAGTG GCACGGGAGG

310 320 330 340 350 360
AGCAGCCTTGG GCACCCAGAC CTACATCTGC AACGTGAATC ACAAGCCCAG CAACACCAAG
TCGTCGAACC CGTGGGTCTG GATGTAGACG TTGCACTTAG TGTTCGGTTC GT'GTGGTTTC

370 380 390 400 410 420
G'GGACAAGA AAGTTGGTGA GAGGCCAGCA CAGGGAGGGA GGGTGTCTGC TGGAAAGCCAG
CACCTGT'TCT T'TCAACCACT CT'CCGGTCGT GTCCCCTCCCT CCCACAGACG ACCCTCGGTC

430 440 450 460 470 480
GCTCAGCGCT CCTGCCTGGA CGCATCCGG CTATGCAGCC CGAGTCCAGG GCAGCAAGGC
CGAGTGGCGA GGACGGACCT GCGTAGGGCC GATACGTCGG GTCAGGTCC CGTGTGTTCC

490 500 510 520 530 540
AGGCCCCGTC TGCCTCTTCA CCCGGAGGCC TCTGCCGCC CCACTCATGC TCAGGGAGAG
TCCGGGCAG ACGGAGAACT GGGCCTCCGG AGACGGGGG GGTGAGTACG AGTCCCTCTC

550 560 570 580 590 600
GGTCTCTGG CTTTTTCCCC AGGGCTCTGGG CAGGCACAGG CTAGGTGCC CTAACCCAGG
CCAGMAGCC GAAAAAGGGG TCCGAGACCC GTCCGTGTC GATCCACGGG GATGGGGTCC

FIGURE 19B
(SEQ ID NO. 23)

pD17-hG1b

610	620	630	640	650	660
CCCTGGCACAC	AAAGGGCCAG	GTGCTGGGCT	CAGACCTGCC	AAGAGCCATA	TCCGGGAGGA
GGGACGTGTG	TTCGGCGTC	CAAGGACCCGA	GTCTGGACGG	TTCCTGGTAT	AGGCCCTCC
670	680	690	700	710	720
CCCTGCCCT	GACCTAAGCC	CACCCAAG	GCCAAACTCT	CCACTCCCTC	AGCTCGGACA
GGGACGGGA	CTGGATTGG	GTGGGTTTC	CGGTTTGAGA	GGTGAGGGAG	TGGAGCCCTGT
730	740	750	760	770	780
CTTCTCTCC	TCCCCAGATTC	CAGTAACCTCC	CAATCTCTC	TCTGCAGAGC	CCAAATCTTG
GGAAAGAGGG	AGGGTCTAACG	GTCAATTGAGG	GTAGAAAGAG	AGACGTTCTCG	GGTTTAGAAC
790	800	810	820	830	840
TGACAAAAT	CACACATGCC	CACCGTGCC	AGGTAAGCCA	GGCCAGGCC	GGCCCTCCAG
ACTGTTTGA	GTGTGTACGG	GTGGCACGGG	TCCATTGGT	GGGTCCGGG	GGGGAGGTG
850	860	870	880	890	900
CTCAAGGGGG	GACAGGTTGCC	CTAGAGTAGC	CTGCATCCAG	GGACAGGCC	CAGCCGGGTG
GAGTTCGGCC	CTGTCCACGG	GATCTCATCG	GACGTAGGTC	CCTGTCCGGG	GTCGGCCCCAC
910	920	930	940	950 z37	960
CTGACACGTC	CACCTCCATC	TCTTCCTCAG	CACCTGAACT	<u>TCTGGGGGA</u>	CCGTCAGTCT
GACTGTGCA	GTGGAGGTAG	AGAAGGAGTC	GTGGACTTGA	<u>GA<u>CC</u>CCCT</u>	GGCACTCAGA
970	980	990	1000	1010	1020
TCTCTTCCC	CCCAAAACCC	AAGGACACCC	TCATGATCTC	CGGACCCCT	GAGGTCACAT
AGGAGAAGGG	GGGTTTGGG	TTCCTGTGGG	AGTACTAGAG	GGCCTGGGA	CTCCAGTGT
1030	1040	1050	1060	1070	1080
GGTGGGTGT	GGACGCTGAGC	CACGAAGACC	CTGAGGTCAA	GTTCAACTGG	TACGTGGACG
CGCACCA	CCTGCACTCG	GTGCTTCTGG	GAATCCAGTT	CAAGTTGACC	ATGCACCTGC
1090	1100	1110	1120	1130	1140
GGTGGAGGT	GCATAATGCC	AAGACAAAGC	CGGGGGAGGA	GCAGTACAAAC	AGCACGTACC
CGCACCTCCA	CGTATTACGG	TTCTGTTTCG	GGGCCCTCC	CGTCATGTTG	TCTGTGCATGG
1150	1160	1170	1180	1190	1200
GTGTGGTCAC	CGTCCTCAC	GTCCCTGCC	AGGACTGGCT	GAATGGCAAG	<u>GA<u>GT</u>AC<u>AA</u>GT</u>
CAACCCAC	GCAGGAGTGC	CAGGACGTGG	TCCTGACCCGA	CTTACCGTTC	<u>CT<u>CA</u>ATG<u>TA</u></u>

FIGURE 19C
(SEQ ID NO. 23)

pD17-hG1b

3' 22	1210	1220	<u>1230</u> 32[1240	1250	1260
GCAAGGTCTC	CAACAAAGCC	CTCCCAGCC	CCATCGAGAA	AACCATCTCC	AAAGCCAAG	
CCTTCCAGAG	GTTGTTTCGG	GAGGGTCCGG	GGTAGCTCTT	TGTTAGAGG	TTCGGTTTC	
1270	1280	1290	1300	1310	1320	
GTCGGACCCG	TGGGTGCGA	GGGCCACATG	GACAGAGGCC	GGCTCGGGCC	ACCCCTCTGCC	
CACCCCTGGCG	ACCCACGGCT	CCCGGTGTAC	CTGTCTCGGG	CCGAGCCGGG	TGGGAGACGG	
1330	1340	1350	1360	1370	1380	
CTGAGAGTGA	CCGCTGTACC	AACCTCTGTC	CCTACAGGGC	AGCCCCGAGA	ACACAGGTG	
GACTCTCAC'T	GGCGACATGG	'TTGGAGACAG	GGATGTCCCCG	TGGGGCTCT	TGGTGTCCAC	
1390	1400	1410	1420	1430	1440	
TACACCCCTGC	CCCCATCCCG	GGATGAGCTG	ACCAAGAAC	AGGTTCAGCCT	GACTTGCCCTG	
ATGTGGGACG	GGGGTAGGGC	CCTACTCGAC	TGGTTCTTGG	TCCAGTGGG	CTGGACGGAC	
1450	1460	1470	1480	1490	1500	
GTCAAAAGGCT	TCTATCCCAG	CGACATCGCC	GTGGAGTGGG	AGAGCAATTGG	GCAGGGGAG	
CAGTTTCCGA	AGATAGGGTC	GCTGTAGGGG	CACCTCACCC	TCTCGTTAAC	CGTCCGGCTC	
1510	1520	1530	1540	1550	1560	
AACAAACTACA	AGACCAACGCC	TCCCGTGGCTG	GACTCCGACG	GCTCCCTCTT	CCTCTACAGC	
TTCGGTTGA'IGT	TCTGGTGGCGG	AGGGCACGAC	CTGAGGCTGCG	CGAGGAAGAA	GGAGATGTG	
1570	1580	1590	1600	1610	1620	
AAGCTCACCG	TGGACAAGAG	CAGGTGGCAG	CAGGGAAACG	TCTTCTCATG	CTCCGTGATG	
TTCGGAGTGGC	ACCTGTTCTC	GTCCACCGTC	GTCCCCRTGC	AGAAGAGTAC	GAGGCACTAC	
1630	1640	1650	1660	1670	1680	
CATGAGGCTC	TGCCACAACCA	CTACACGGCAG	AAGAGCTCT	CCCTGTCTCC	GGGTAATGAA	
GTACTCCGAG	ACGTGTTGGT	GATGTGGCTC	TTCTCGGAGA	GGGACAGAGG	CCCATTTACT	
1690	1700	1710	1720	1730	1740	
GTGGGACGCC	CGGCAAGCCC	CGGCTCCCCG	GGCTCTCGCG	GTGCGACGAG	GATGGCTGGC	
CACGCTGCCG	GGCGTTCGGG	GGCGAGGGGC	CCGAGAGGCC	CAGCGTGGCTC	CTACGAACCG	
1750	1760	1770	1780	1790	1800	
ACGTACCCCC	TGTACATACT	TCCCCGGCGC	CCAGGCATGGGAA	ATAAAAGCAC	CCAGCGCTGCG	
TGCAATGGGG	ACATGATGA	AGGGCCCGCG	GGTCGTACCT	TATATTGCGT	GGTCGGGACG	

FIGURE 19D
(SEQ ID NO. 23)

pD17-hG1b

1810	1820	1830	1840	1850	1860
CCTGGCCCC	TGCCAGAC'G	TGATGGTTCT	TTCACGGGT	CAGGCCGAGT	CTGAGGCCTG
GGACCGGGG	ACGCTCTGAC	ACTACCAAGA	AAGGTGCCA	GTCGGGCTCA	GACTCCGGAC
1870	1880	1890	1900	1910	1920
AGTGGCATGA	GGGAGGCAGA	GGGGTCCCAG	CTGTCCCAC	ACTGCCAG	GCTGTGCAGG
TACACCGTACT	CCCTCCGTCT	CGCCCAAGGGT	GACAGGGGTG	TGACCGGGTC	CGMACACGTCC
1930	1940	1950	1960	1970	1980
TGTGCCCTGG	CCCCCTAGGG	TGGGCTCAG	CCAGGGGCTG	CCCTCGGCAG	GGTGGGGGAT
ACACCGGACCC	GGGGGATCCC	ACCCCGAGTC	GGTCCCGAC	GGGAGCCGTC	CCACCCCCTA
1990	2000	2010	2020	2030	2040
TGCCAGGGT	GGCCCTCCCT	CCAGCAAGCAC	CTGGCCCTGGG	CTGGGCCACG	GGAAAGCCCTA
AACGGTGCAC	CCGGGAGGGA	GGTCGTCTGT	GACGGGACCC	GACCCGGTGC	CCTTCGGGAT
2050	2060	2070	2080	2090	2100
GGAGGCCCTG	GGGACAGACA	CACAGCCCCCT	GCCTCTGTAG	GAGACTGTCC	TGTTCCTGTGA
CCTCGGGGAC	CCCTGTCTGT	GTGTGGGGA	CGGAGACATC	CTCTGACAGG	ACAAGACACT
2110	2120	2130	2140	2150	2160
GCCCCCTGT	CCTCCCGACC	TCCATGCCA	CTCGGGGCCA	TGCTGGGAT	GGGGTGGGCT
CGGGGGACCA	GGAGGGCTGG	AGGTACGGGT	GAGCCCCCGT	ACGACCCCTA	CGCCACCCGA
2170	2180	2190	2200	2210	2220
C'TATGGC'TC	TGAGGGGGAA	AGAACAGCT	GGGGCT'AG	GGGGTATCCC	CACGGCCCT
GATAACCGAAG	ACTCCGCCTT	TCTTGTCGA	CCCCGAGATC	CCCCATAGGG	G'GGGGGGGA
2230	2240	2250	2260	2270	2280
GTAGGGGGC'	ATTAAGCGCG	GGGGGTGTGG	TGGTTACGCG	CAGCGTACCC	GCTACACTTG
CAT'CGCCGG	TAATTGCGCG	CGCCCAACACC	ACCAATGCGC	GTGCGACTGG	CGATGTGAAC
2290	2300	2310	2320	2330	2340
CCAGGGCCCT	AGCCGCCGCT	CCTTTCGCTT	TCTTCCCTTC	CTTCTCGCC	ACGTTCGCCG
GGTGGGGGA	TCGGGGCGA	GGAAAGCGAA	AGAAAGGAAG	GAAAGAGGG	TGCAAAGCGGC
2350	2360	2370	2380	2390	2400
GCTTTCGGCG	TCAAGGCTCTA	AATCGGGGCA	TCCCTTTAGG	GTTCGGATT	AGTGCTTTAC
CGAAAGGGCC	AGTTCGAGAT	TTAGCCCCGT	AGGAAATCC	CAAGGCTAAA	TCACGAAATG

FIGURE 19E
(SEQ ID NO. 23)

pD17-hG1b

2410	2420	2430	2440	2450	2460
GGCACCTCGA	CCCCAAAAAA	CTTGATTAGG	GTGATGGTTC	ACGTAGTGGG	CCATCGCCCT
CCGTGGAGCT	GGGGTTTTTT	GAACTAATCC	CACTACCAAG	TGCATCACC	GGTAGGGGA
2470	2480	2490	2500	2510	2520
GATAGACGGT	TTTCGCCCT	TTGACGTTGG	AGTCCACGTT	CTTTAATACT	GGACTCTTGT
CTATCTGCCA	AAAAGGGGA	AACTGCAACC	TCAGGTGCAA	GAATTATCA	CCTGAGAACAA
2530	2540	2550	2560	2570	2580
TCCAAACATGG	AACAAACACTC	AACCCTATCT	CGGTCTATTTC	TTTIGATTAA	TAACGGATT
AGGTTTGACC	TRGTTGTGAG	TRGGGATAGA	GCCAGATAAG	AAAACTAAAT	ATTCCTAAAA
2590	2600	2610	2620	2630	2640
TGGGGATTTC	GGCCTATTGG	TTAAAAAAATG	AGCTGATTAA	ACAAAAAATT	AACGGGAATT
ACCCCTAAAG	CCGGATAACC	AATTTTTAC	TCGACTAAAT	TGTTTTTAA	TGCGCTTAA
2650	2660	2670	2680	2690	2700
ATTCCTGTGG	AATGGTGTGTC	AGTTAGGGTG	TGGAAAGTCC	COAGGGCTCCC	CAGGCAGGCA
TTAAGACACC	TTACACACAG	TCAATCCAC	ACCTTTCAGG	GGTCCCGAGG	GTCCGTCCCGT
2710	2720	2730	2740	2750	2760
GAAGTATGCCA	AAGCATGCCAT	CTCAATTAGT	CAGCAACCAT	AGTCCCGCCC	CTAAACTCCGC
CTTCATACGTT	TTCGTACGTA	GAGTTAAATCA	GTCTTGGTA	TCAGGGGGGG	GATTGAGGGCG
2770	2780	2790	2800	2810	2820
CCATCCGCC	CCTAAACTCCG	CCCAGTTCCG	CCCATTCCTCC	GCCCCATGGC	TGACTAATT
GGTAGGGCGG	GGATTGAGGC	GGGTCAAGGC	GGGTAAGAGG	CGGGGTACCG	ACTGATTAA
2830	2840	2850	2860	2870	2880
TTTTTATTAA	TGCAGAGGCC	GAGGCCGCCT	CGGCCCTCTGA	GCTATTCCAG	AAGTAGTGAG
AAAATAAATT	ACGTCTCCGG	CTCCGGGGAA	GCCGGAGACT	CGATAAGGTC	TTCATCACTC
2890	2900	2910	2920	2930	2940
GAGGCTTTT	TGGAGGCCTA	GGCTTTTGCA	AAAAGCTTGG	ACAGCTCAGG	GCTGGATTT
CTCCGAAAAA	ACCTCCGGAT	CCGAAACGT	TTTCGAAACC	TGTCGAGTCC	CGACGGCTAA
2950	2960	2970	2980	2990	3000
CGGCCAAAC	TTCGACGGCAA	TCCTAGCGTG	AAGGGCTGGTA	GGATTCTATC	CCCGCTGCCA
GGCGGGTTTG	AACTGCCGTT	AGGATGCCAC	TTCCGACCAT	CCTAAATAG	GGCGACGGT

FIGURE 19F
(SEQ ID NO. 23)

pD17-hG1b

3010	3020	3030	3040	3050	3060
TCATGGT'TCG	ACCAT'TGAAAC	TGCATCGTCG	CCGTGTCCTCA	AAATAATGGGG	ATGGCAAGA
AGTACCAAGC	TGGTAAC'TG	ACGTAGCAGC	GGCACAGGGT	TTTATACCCC	TAACCGTTCT
3070	3080	3090	3100	3110	3120
ACGGAGACT'	ACCTGGCCT	CCGCTCAGGA	ACGAGTCTCAA	GTACTTCCAA	AGAATGACCA
TGCCCTCTGCA	TGGGACCGGA	GGCGAGTCCT	TGCTCAAGTT	CATGAAGGTT	TCTTACTGGBT
3130	3140	3150	3160	3170	3180
CAACCTCTTC	AGTGGAAAGT	AAACAGAAATC	TGGTGATTAT	GGTAGGGAAA	ACCTGGTTCT
GTTGGAGAAG	TCACCTTCCA	TTTGTCTTAG	ACCACTAATA	CCCATCCTTT	TGGACCAAGA
3190	3200	3210	3220	3230	3240
CCATTCCTCGA	GAAGAAATCGA	CCTTAAAGG	ACAGAAATTAA	TATAGTTCTC	AGTAGAGAAC
GGTAAGGACT'	C'TTCTTAGCT	GGAAATTTC	TGTCTTAATT	ATATCAAGAG	TCATCTCTTG
3250	3260	3270	3280	3290	3300
TCAAAGAAC	ACCAACGAGGA	GCTCATTTTC	TTGCCAAAAAG	TTTGGATGAT	GCCTTAAGAC
AGTTTCTTGG	TGGTGCTCCT	CGAGTAAAG	AACGGTTTC	AAACCTACTA	CGGAATTCTG
3310	3320	3330	3340	3350	3360
TTATTGACA	ACCGGAATTG	GCAAGTAAAG	TAGACATGGT	TTGGATAAGTC	GGAGGCAGTT
ATAACTTGT	TGGCCTAAC	CGTTCATTTC	ATCTGTACCA	AACTTATCAG	CCTCCGTCAA
3370	3380	3390	3400	3410	3420
CTGTTACCA	CGAAGCCATG	AATCAACCAG	GCCACCTTAG	ACTCTTTGTG	ACAAGGATCA
GACAAATGGT'	CCTTCGGTAC	TTAGTTGGTC	CGGTGGAATC	TGAGAAACAC	TGTTCCCTAGT
3430	3440	3450	3460	3470	3480
TGCAGGAAATT'	TGAAGTGTGAC	ACGTTTTTC	CAGAAATTGA	TTTGGGGAAA	TATAAAACTC
ACGTCCTTAA	ACTTTCACTG	TGCAAAAGG	GTCTTAACT	AAACCCCTT	ATATTGAG
3490	3500	3510	3520	3530	3540
TCCCAGAAATA	CCCAGGGTGC	CTCTCTGAGG	TCCAGGAGGA	AAAAGGCATC	AAGTATAAGT
AGGGTCTTAT	GGTCCCGCAG	GAGAGACTCC	AGGTCTCCT	TTTTCGGTAG	TTCATATTCA
3550	3560	3570	3580	3590	3600
TTGAAGTCTA	CGAGAAAGAA	GACTAACAGG	AAGATGCTTT	CAAGTTCTCT	GCTCCCCCTCC
AACTTCAGAT'	GCTCTTCTT	CTGATTGTCC	TTCTACGAAA	GTTCAAGAGA	CGAGGGGAGG

FIGURE 19G
(SEQ ID NO. 23)

pD17-hG1b

3610 3620 3630 3640 3650 3660
TAAAGCTATG CATTTTATA AGACCATGGG ACTTTTGCTG GCTTTAGTC TCTTTGTGAA
ATTTCGATAC GTAAAAAATAT TCTGGTACCC TGAAAACGAC CGAAATCTAG AGAAACACTT
3670 3680 3690 3700 3710 3720
GGAACCTTAC TTCTGTGGTG TGACATAATT GGACAAACTA CCTACAGAGA TTAAAGCTC
CCTTGGAAATG AAGACACCAC ACTGTATTAA CCTGTTGAT GGATGTCCT AAATTCGAG
3730 3740 3750 3760 3770 3780
TAAGGTAAT ATAAAATT TTAAAGTGTATA ATGTGTAAA CTACTGATTC TAATTTGTGTTG
ATTCCATTAA TATTTTAAA ATTACACATAT TACACATTG GATGACTAAG ATTAACAAAC
3790 3800 3810 3820 3830 3840
TGATATTAG ATTCCAACTT ATGGAACCTG TGAATGGAG CAGTGGTGA ATGCCCTTAA
ACATAAAATC TAAGGTTGGA TACCTGTACT ACTTACCTC GTCACCACCT TACGGAAATT
3850 3860 3870 3880 3890 3900
TGAGGAAAAC CTGTTTGCT CAGAAGAAAT GCCATCTAGT GATGATGAGG CTACTGCTGA
ACTCCTTTTG GACAACCGA GTCTTCTTTA CGGTAGATCA CTACTACTCC GATGACGACT
3910 3920 3930 3940 3950 3960
CTCTCAACAT TCTACTCCTC CAAAAAGAA GAGAAAGGTAA GAAGACCCCA AGGACTTTCC
GAGAGTTGTA AGATGAGGAG GTTTTCTT CTCTTCCAT CTCTCTGGGT TCCTGAAAGG
3970 3980 3990 4000 4010 4020
TTAGAATTG CTAAGTTTT TGAGTCATGC TGTGTTTAGT ATAGAAACTC TTGCTTGCT
AAGTCTAAC GATTCAAAA ACTCAGTACG ACACAAATCA TTATCTTGAG AACGAAACGAA
4030 4040 4050 4060 4070 4080
TGCCTATTAC ACCACAAAGG AAAAAGCTGC ACTGCTATAC AAGAAAATTAA TGAAAATA
ACGATAAATG TGGTGTTC CCGTATGTG TGACGATATG TTCTTTTAAT ACCTTTTAT
4090 4100 4110 4120 4130 4140
TTCTGTAACC TTTATAAGTA GGCATAACAG TTATAATCAT AACATACTGT TTTTCTTAC
AAGACATGG AAATATTCAAT CCGTATGTG AATATTAGTA TTGTATGACA AAAAAGAATG
4150 4160 4170 4180 4190 4200
TCACACAGG CATAGAGTGT CTGCTATTAA TAACTATGCT CAAAATTGT GTACCTTTAG
AGGTGTGTCG GTATCTCACAA GACGATTAATT ATTGATACGA G'TTTTAACAA CATGAAATC

FIGURE 19H
(SEQ ID NO. 23)

pD17-hG1b

4210 4220 4230 4240 4250 4260
CTTTTAATT TGAAAGGGG TTAATAAGGA ATATTTGATG TATAGTGCCT TGAAGAGA
GAAAATTAA ACATTTCCCC AATTATTCCCT TATAACTAC ATATCACGGA ACTGATCTC

4270 4280 4290 4300 4310 4320
TCATAATCAG CCATACCACA TTGTAGAGG TTTTACTTGC TTTAAAAAAC CTOCCCACACC
AGATAATTAGTC GGTATGGTGT AAACATCTCC AAAATGAAACG AAATTTTTG GACGGGTGTGG

4330 4340 4350 4360 4370 4380
TCCCCCTGAA CCTGAAACAT AAAATGAATG CAATTGTTGT TGTTAACCTTG TTATTGCGAG
AGGGGCACCTT GGACTTGTAA TTTTACTTAC GTTAACAAACA ACAATTGAAAC AAATAACGTC

4390 4400 4410 4420 4430 4440
CTTATAATGG TTACAAATAA AGCAATAGCA TCACAAATT CACAAATAAA GCATTTTTT
GAATATTACCA AATGTTTATT TCGTTATCGT AGTGTTTAAA GTGTTTATT CGTAAAAAAA

4450 4460 4470 4480 4490 4500
CACTGCATTC TAGTTGTTGT TTGTCCAAC TCATCAATGT ATCTTATCAT GTCTGGATCG
GTGACCTAAG ATCAAACACCA AACAGGTTTG AGTAGTTACA TAGAATAGTA CAGACCTAGC

4510 4520 4530 4540 4550 4560
GCTGGATGAT CCTCCAGGGC GGGGATCTCA TGCTGGAGTT CTTGCCAC CCCAACTTGT
CGACCTACTA GGAGGTGGCG CCCCTAGAGT ACGACCTCAA GAAGGGGTG GGGTTGAACA

4570 4580 4590 4600 4610 4620
TTATTGCAGC TTATAATGGT TACAAATAAA GCAATAGCAT CACAAATTTC ACAAAATAAAG
ATAAACGTCG AATATTACCA ATGTTTATT CGTTATCGTA GTGTTAAAG TGTTTATTTC

4630 4640 4650 4660 4670 4680
CAATTTC ACTGCATTCT AGTTGTTGT TGTCCAACAT CATCAATGTA TCTTATCATG
GTTAAAAAG TGACGTAAGA TCAACACCAA ACAGGTTTGA GTAGTTACAT AGAATAGTAC

4690 4700 4710 4720 4730 4740
TCTGTATACC GTGGACCTCT AGCTAGAGCT TGGCGTAATC ATGGTCATAG CTGTTTCCCTG
AGACATATGG CAGCTGGAGA TCGATCTCGA ACCGCATTAG TACCAAGTATC GACAAAGGAC

4750 4760 4770 4780 4790 4800
TGTGAATTG TTATCCGCTC ACAATTCCAC AACACATACG AGCCGGAAAGC ATAAAGTGTAA
ACACTTAAAC AATAGGGAG TGTAAAGGTG TGTGTATGCC TCGGCCTTCG TATTTTCACAT

FIGURE 19I
(SEQ ID NO. 23)

pD17-hG1b

4810	4820	4830	4840	4850	4860
AAGCCTGGG	TGCCCTAATGA	GtgAGCTAAC	TCACATTAAT	TGGCTTGC	TCACTGCC
TTCGGACCC	ACGGATTACT	CACTCGATTG	AGTGTAAATTA	ACGCAACGGG	AGTGACGGGC
4870	4880	4890	4900	4910	4920
CTTTCAGTC	GGGAAACCTG	TGTTGCCAGC	TGCATAATG	ATCGGCCAA	CGGCCGGGA
GAAAGGTAG	CCCTTGGAC	AGCACGGTCG	ACGTAATTAC	TAGCCGGTT	GGCGCCCT
4930	4940	4950	4960	4970	4980
GAGGGGGTTT	GGGTATTGGG	CGCTCTTCCG	CTTCCTCGCT	CACTGACTCG	CTGCGCTCGG
CTCCGCCAA	CGCATAAACCC	GCGAGAAAGGC	GAAGGAGCGA	GTGACTGAGC	GACGGAGGCC
4990	5000	5010	5020	5030	5040
TCCGTTGGCT	GGGGCGAGCG	GTATCAGCTC	ACTCAAMGGC	GGTAATAACGG	TTATCCACAG
AGCAAGCCG	CGCCGCTCGC	CATAGTCGAG	TGAGTTCCG	CCATTATGCC	AATAGGTGTC
5050	5060	5070	5080	5090	5100
AATCAGGGG	TAACGCCAGGA	AAGAACATGT	GAGCAAAGG	CCAGCAAAAG	GCCAGGAACCC
TTAGTCCCCCT	ATTGCGTCCT	TTCTTGTACA	CTCGTTTCC	GGTCGTTTC	CGGTCCCTTGG
5110	5120	5130	5140	5150	5160
GTAAAAAGGC	CGCGTTGCTG	GGTTTTTCC	ATAGGCTCCG	CCCCCCTGAC	GAGCATCACAA
CATTTTCCG	GGCAACACGAC	CGCAAAAGG	TATCGAGGC	GGGGGACTG	CTCGTAGTGT
5170	5180	5190	5200	5210	5220
AAAATCGACG	CTCAAGTCAG	AGGTGGCGAA	ACCCGACAGG	ACTATAAGA	TACCAAGGCGT
TTTTAGCTGC	GAGTTCAGTC	TCCACCGCTT	TGGGCTGTCC	TGATATTCT	ATGGTCCCGCA
5230	5240	5250	5260	5270	5280
TTCGGCCCTG	AAGCTCCCTC	GTGGCGTCTC	CTGTTCCGAC	CTGGCCGCTT	ACCGGATAACC
AAGGGGGAC	TTCGAGGGAG	CACGGAGAG	GACAAGGCTG	GGACGGGAA	TGGCCTATGG
5290	5300	5310	5320	5330	5340
TGTCCGCCTT	TCTCCCTTCG	GGAAAGGTGG	CGCTTCTCA	ATGCTCACGC	TGTAGGTATC
ACAGGGGAA	AGAGGGAAAGC	CCTTCCGACC	GGAAAGAGT	TACGAGTGGC	ACATCCATAG
5350	5360	5370	5380	5390	5400
TCAGTTGGT	GTAGGTGTT	CGCTCCAAGC	TGGGCTGTGT	GCACGAACCC	CCCGTTCAAG
AGTCAGGCCA	CATCCAGCAA	GGAGGTTCG	ACCCGACACA	CGTGCTTGGG	GGGCAAGTCC

FIGURE 19J
(SEQ ID NO. 23)

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5410	5420	5430	5440	5450	5460
CCGACCGCTG	CGCCTTATCC	GGTAACTATC	GTCCTGAGTC	CAACCCGGTA	AGACACGACT
GGCTGGCGAC	GGGAAATAGG	CCATTGATAG	CAGAACCTCAG	GTTGGGCCAT	TCTGTGCTGA
5470	5480	5490	5500	5510	5520
TATCGCCACT	GGCAGCAGCC	ACTGTTAACCA	GGATTAGCAG	ACCGAGGTAT	GTAGGGGGTG
ATAGCGGTGA	CGGTGCGTGG	TGACCATTTGT	CCTAATCGTC	TCGCTCCATA	CATCCGCCAC
5530	5540	5550	5560	5570	5580
CTACAGAGTCT	CTTGAAGTGG	TGGCCTAACT	ACGGCTACAC	TAGAAGGACA	GTATTITGGCTA
GATGTCCTCAA	GAACCTCACCC	ACCGGATTGA	TGCCGATGTCG	ATCTTCCCTGT	CATAAACCAT
5590	5600	5610	5620	5630	5640
TCTGCCCTCT	GCTGAAGCCA	GTTACCTTCG	GAAAAGAGT	TGGTAGGCTCT	TGATCCGGCA
AGACGGAGA	CGACTTCGGT	CAATGGAAGC	CTTTTCTCA	ACCATGGAGA	ACTAGGCCGT
5650	5660	5670	5680	5690	5700
AACAAACAC	CGCTGGTAGC	GGTGGTTTT	TTGTTTGCAA	GCAGCAGATT	ACGGCAGAA
TGTTTGGTG	GGCACCATCG	CCACCAAAA	AACAAACGTT	CGTCGTCATA	TGCGCGTCTT
5710	5720	5730	5740	5750	5760
AAAAGGATC	TCAAGAAGAT	CCTTGTATCT	TTTCTACGGG	GTCTGACGCT	CAGTGGAAACG
TTCCTCTAG	AGTCTCTCTA	GGAAACTAGA	AAAGATGCC	CAGACTGCGA	GTACACCTTGC
5770	5780	5790	5800	5810	5820
AAAACTCAG	TTAAGGGATT	TTGGTCATGA	GATTATCAA	AAGGATCTTC	ACCTAGATCC
TTTTGAGTCC	AATTCCCTAA	AACCAGTACT	CTAATAGTTT	TTCCCTAGAAG	TGGATCTAGG
5830	5840	5850	5860	5870	5880
TTTTAAATTAA	AAAATGAAGT	TTTAAATCAA	TCTAAAGTAT	ATATGAGTAA	ACTTGGTCTG
AAAATTAAAT	TTTTACTTCA	AAATTAGTT	AGATTCTATA	TATACTCATT	TGAACCAGAC
5890	5900	5910	5920	5930	5940
ACAGTTACCA	ATGCTTAAATC	AGTGAGGCAC	CTATCTCAGC	GATCTGTCTA	TTTCGTTCTAT
TGTCAATGGT	TACGAATTAG	TCACTCCGTG	GATAGAGTCG	CTAGACAGAT	AAAGCAAGTA
5950	5960	5970	5980	5990	6000
CCATAGTTGC	CTGACTCCCC	GTCTGTTAGA	TAACCTACGAT	ACGGGAGGGC	TTACCATCTG
GGTATCAG	GACTGAGGGG	CAGCACATCT	ATTGATGCTA	TGCCCTCCCG	AAATGGTAGAC

FIGURE 19K
(SEQ ID NO. 23)

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6010	6020	6030	6040	6050	6060
GCCCCAGTGC	TGCAATGATA	CCGGCAGACC	CACGCTCACC	GGCTCCAGAT	TTATCAGCAA
CGGGGTCA CG	ACGTTACTAT	GGCGGTCTGG	GTGGGAAGTGG	CCGAGGTCTA	AATAGTCGTT
6070	6080	6090	6100	6110	6120
TAAACCAGCC	AGCCGGAAGG	GCCGAGGCCA	GAAGTGGTCC	TGCAACTTAA	TCCGCCCTCCA
ATTGGTCGG	TGGGCCCTTC	CGGCTCGCGT	CTTCACCAAGG	ACGTTGAAAT	AGGGGGAGGT
6130	6140	6150	6160	6170	6180
TCCAGTCTAT	TAATTGTTGC	CGGGAAAGCTA	GAGTAAGTAG	TTCGCCAGTT	AATAGTTTGC
AGGTCA GATA	ATTAACAACG	GCCCTTCGAT	CTCATTCATC	AAGGGTCAA	TTATCAAACG
6190	6200	6210	6220	6230	6240
GCAAACGTTGT	TGCCATTGCT	ACAGGGCATCG	TGGTGTACG	CTCGTGTCTT	GGTATGGCTT
C GTTGC AACA	ACGGTAACGA	TGTCCGTAGC	ACCACAGTGC	GAGCAGCAA	CCATACCGAA
6250	6260	6270	6280	6290	6300
CATT CAGGCTC	CGGTTCCAA	CGATCAAAGGC	GAGTTACATG	ATCCCCCATG	TTGTGCAA
GTAAAGTCGAG	GCCAAAGGGT	GCTAGTTCCG	CTCAATGTAC	TAGGGGGTAC	AACACGTTT
6310	6320	6330	6340	6350	6360
AGGCGGTTAG	CTCCCTTCGGT	CCTCCCGATCG	TTGTCAAGAAG	TAAGTTGGCC	GCAGTGTAT
TTCGCCAATC	GAGGAAGCCA	GGAGGCTAGC	AACAGTCTTC	ATTCAACCGG	CGTCACAATA
6370	6380	6390	6400	6410	6420
CACTCATGGT	TATGGCAGCA	CTGCATAATT	CTCTTACTGT	CATGCCATCC	GTAAGATGCT
G'GAGTACCA	ATACCGTCTGT	GACGTATTA	GAGAATGACA	GTACGGTAGG	CATCTACGA
6430	6440	6450	6460	6470	6480
T'TCTGTGAC	TGGTGAGTAC	TCAACCAAGT	CATTCTGAGA	ATAGTGTATG	CGCGAACCGA
AAAGACACTG	ACCACTCATG	AGTTGGTTCA	GTAAGACTCT	TATCACATAC	GCCGCTGGCT
6490	6500	6510	6520	6530	6540
G'TGCTCTTG	CCGGCGTCA	ATACGGATA	ATACCGGCC	ACATAGCAGA	ACTTTAAAAG
CAACGAGAAC	GGGCCCGACT	TATGCCCTAT	TATGGGCCGG	TGTATCGTCT	TGAATTTTC
6550	6560	6570	6580	6590	6600
TGCTCATCAT	TGGAAAACGT	TCTTCGGGGC	GAAAACCTCTC	AAGGATCTTC	CCGCTGTCTA
ACGAGTAC'A	ACCTTTGCA	AGAACCCCCG	CTTTTGAGAG	TTCCTAGAAT	GGCGACAACT

FIGURE 19L
(SEQ ID NO. 23)

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6610 6620 6630 6640 6650 6660
GATCCAGTTC GATGTAACCC ACTCGTGCAC CCAACTGATC TTCAGCATCT TTTACTTTCA
CTAGGTCAAG CTACATTGGG TGAGCACGTG GGTTGACTAG AAGTCGTAGA AAATGAAGT
6670 6680 6690 6700 6710 6720
CCAGCGT'TTC TGGGTGAGCA AAAACAGGAA GGCAAAATGC CGCAAAAAAG GGAATAAGGG
GGTGGCAAAG ACCCAACTCGT TTGTTGTCCTT CGGTTTACG GCGTTTTTC CCTTATTCCC
6730 6740 6750 6760 6770 6780
CGACACGGAA ATGTTGAATA CTCATACTCT TCCTTTTCA ATATTATTGA AGCATTATC
GCTGTGCCCT TACAACATT GAGTATGAGA AGGAAAAGT TATAATACT TCGTAAATAG
6790 6800 6810 6820 6830 6840
AGGCGTTATTG TCTCATGAGC GGATACATAT TTGAAATGTAT TTGAAAAAAT AAACAAATAG
TCCAATAAC AGAGTACTCG CCTATGTATA AACTTACATA ATCTTTTTA TTGTTTATC
6850 6860 6870 6880 6890 6900
GGGTTCCGCG CACATTTCCC CGAAAAGTGC CACCTGACGT CGACGGATCG GGAGATCTGC
CCCAGGGCGC GTGTAAGGG GCTTTTCACG GTGGACTGCA GCTGCCTAGC CCTCTAGACG
6910 6920 6930 6940 6950 6960
TAGGTGACCT GAGGCGCGCC GGCTTCAATT AGCCACAGATA ACCTTTTTT TTAAATTTT
ATCCACTGGA CTCCGGCGGG CCGAAGCTTA TCGGTCTCAT TGAAAAAAA ATTAAAAATA
6970 6980 6990 7000 7010 7020
TTTATTATT TTTTGAGATG GAGTTGGCG CCGATCTCCC GATCCCCAT GGTGACTCT
AAATAAAATA AAACACTCTAC CTCAAACCGC GGCTAGAGGG CTAGGGATA CCAGCTGAGA
7030 7040 7050 7060 7070 7080
CACTACAATC TGCTCTGATG CCGCATAGTT AAGCCAGTAT CTGCTCCCTG CTGCTGTGT
GTCATGTTAG ACGAGACTAC GGGGTATCAA TTGGTCAAA GACGAGGGAC GAACACACAA
7090 7100 7110 7120 7130 7140
GGAGGTGGCT GAGTACTGCG CGAGCAAAAT TTAAGCTACA ACAAGGCAAG GCTTGACCGA
CCTCCAGGGAA CTCATCACGC GCTCGTTTA AATTGATGT TGTTCGGTTC CGAACCTGGCT
7150 7160 7170 7180 7190 7200
CAATTGCATG AAGAAATCTGC TAGGGTTAG GCGTTTGCG CTGCTTCGGC ATGTAACGGGC
GTTAACCTAC TCTCTTAGACG AATCCCAATC CGCAAAACGC GACGAAGGGC TACATGCCCG

FIGURE 19M
(SEQ ID NO. 23)

pD17-hG1b

7210 7220 7230 7240 7250 7260
CAGATATA CGTGACAT GATTGGAC TAGTTATAA TAGTAATCAA TTACGGGGTC
GTCTTATAGC GCAACTGTAA CTAATAACTG ATCAATAATT AICATTAGTT AATGCCCAAG
7270 7280 7290 7300 7310 7320
ATTAGTTCAT AGCCCATATA TGGAGTTCCG CGTTACATAA CTTACGGTAA ATGGCCCGCC
TAATCAAGTA TCGGGTATAT ACCTCAAGGC GCAATGTATT GAATGCCATT TACCGGGCGG
7330 7340 7350 7360 7370 7380
TGGCTGACCG CCCAACGACC CCCGCCATT GACGTCATAA ATGACGTATG TTCCCATAGT
ACCGAC'RGCC GGGTTGCTGG GGGGGTAA CTGCAGTTAT TACTGCATAC AACGGTATCA
7390 7400 7410 7420 7430 7440
AACGCCAATA GGGACTTTCC ATTGACGTCA ATGGGTGGAC TATTGTACGGT AAACCTGCCA
TGGCGGTAT CCCTGAAAGG TAATGCACT TACCCACCTG ATAAATGCCA TTTGACGGGT
7450 7460 7470 7480 7490 7500
CTTGGCAGTA CNTCAAGTGT ATCATATGCC AAGTACGCC CCTATTGACG TCAATGACGG
GAACCGTCA GTAGTTACA TAGTATACGG TTCATGGGG GGATAACTGC AGTTACTGCC
7510 7520 7530 7540 7550 7560
TAAATGGCCC GCCTGGCATT ATGCCCAAGTA CATGACCTTA TGGGACTTTC CTACTTGGCA
ATTACCGGG CGGACCGTAA TACGGGTCA GTACTGGAAT ACCCTGAAAG GATGAACCGT
7570 7580 7590 7600 7610 7620
GTACATCTAC GTATTAGTCA TCGCTATTAC CATGGTGTATG CGGTTTTGGC AGTACATCAA
CATGTAGATG CATAATCAGT AGCGATAATG GTACCACTAC GCCAAAACCG TCATGTAGTT
7630 7640 7650 7660 7670 7680
TGGCGGTGGA TAGCGGTTTC ACTCACGGGG ATTTCACAAAGT CTCCACCCCA TTGACGTCAA
ACCCGCAC'AT ATCCGCCAAC TGAGTGGCCC TAAAGGTTCA GAGGTGGGT AACITGCAGTT
7690 7700 7710 7720 7730 7740
TGGGACTT'TG TTTGGCACC AAAATCAACG GGACTTTCCA AAATGTCGTA ACAACTCCGC
ACCCCTCAAAC AAAACCGTGG TTTTAGTTGC CCTGAAAGGT TTTACACGCCAT TGTGTAGGGCG
7750 7760 7770 7780 7790 7800
CCCATGGACG CAAATGGGGG GTAGGGCGTGT ACGGTGGGAG GTCTATATAA GCAGAGGCTCT
GGCTAAC'TGC CT'TACCCGC CATCCGCACA TGCCACCTC CAGATATATT CG'CTCGAGA

FIGURE 19N
(SEQ ID NO. 23)

pD17-hG1b

7810 7820 7830 7840 7850 7860
CTGGCTAACT AGAGAACCAA CTGCTTACTG GCTTTATCGAA ATTAAATACGA CTCACTATAAG
GACCAGATTGA TCTCTTGCGGT GACGAAATGAC CGAATAGCTT TAATTATGCT GAGTGATATC

7870 7880
GGAGAACCAA GCTT
CCTCTGGGTT CGAA

Figure 26

hBR96-2 Heavy Chain Variable Region (V_H)

1 EVQLVESGGG 11 LVQPGGSLRL 21 SCAASGFPPFS 31 DYYMYWVRQA 41 PGKGLEWVSY
51 ISQDGDDITDY 61 ADSVKGRFTI 71 SRDNAKNSLY 81 LQMNSLRDED 91 TAVYYCARGL
101 ADGAWEAYWG 111 QGTLVTVSS (SEQ ID NO. 24)

human IgG1 constant

|^{CH1} STKGPSVFPL APSSKSTSGG TAALGCLVKD
YFPEPVTVSW NSGALTSGVH TFPAVLQSSG LYSLSSVVTV PSSSLCTQTY
ICNVNHKPSN TKVDKKVEPK SCDKTHTCPP C^{CH2}A¹³⁵S¹³⁷ P¹³⁸ SVFLFPPKPK
DTLMISRTPE VTCVVVDVSH EDPEVKFNWY VDGVEVHN^{AK} TKPREEQYNS
TYRVVS³¹⁸ V³²⁰ L³²² H³²⁴ Q³²⁶ VSNKAL P³²⁸ EKTISK A³²⁹ K³³¹ Q³³³ P³³⁵ R³³⁷ E³³⁹ P³⁴¹ Q³⁴³ P³⁴⁵ Q³⁴⁷ V³⁴⁹ P³⁵¹ Q³⁵³ V³⁵⁵ P³⁵⁷ Q³⁵⁹ V³⁶¹ P³⁶³ Q³⁶⁵ V³⁶⁷ P³⁶⁹ K³⁷¹ P³⁷³ E³⁷⁵ T³⁷⁷ I³⁷⁹ S³⁸¹ K³⁸³ T³⁸⁵ P³⁸⁷ P³⁸⁹ V³⁹¹ P³⁹³ V³⁹⁵ L³⁹⁷ P³⁹⁹ D⁴⁰¹ G⁴⁰³ S⁴⁰⁵ F⁴⁰⁷ F⁴⁰⁹ L⁴¹¹ Y⁴¹³ S⁴¹⁵ F⁴¹⁷ L⁴¹⁹ Y⁴²¹ W⁴²³ G⁴²⁵ T⁴²⁷ V⁴²⁹ S⁴³¹ L⁴³³ R⁴³⁵ K⁴³⁷ S⁴³⁹ R⁴⁴¹ W⁴⁴³ Q⁴⁴⁵ V⁴⁴⁷ S⁴⁴⁹ V⁴⁵¹ M⁴⁵³ S⁴⁵⁵ P⁴⁵⁷ G⁴⁵⁹ K⁴⁶¹ L⁴⁶³ V⁴⁶⁵ K⁴⁶⁷ H⁴⁶⁹ N⁴⁷¹ Y⁴⁷³ H⁴⁷⁵ T⁴⁷⁷ P⁴⁷⁹ V⁴⁸¹ V⁴⁸³ P⁴⁸⁵ V⁴⁸⁷ S⁴⁸⁹ V⁴⁹¹ M⁴⁹³ H⁴⁹⁵ N⁴⁹⁷ Y⁴⁹⁹ H⁵⁰¹ T⁵⁰³ P⁵⁰⁵ V⁵⁰⁷ V⁵⁰⁹ P⁵¹¹ V⁵¹³ S⁵¹⁵ V⁵¹⁷ M⁵¹⁹ H⁵²¹ N⁵²³ Y⁵²⁵ H⁵²⁷ T⁵²⁹ P⁵³¹ V⁵³³ V⁵³⁵ P⁵³⁷ V⁵³⁹ S⁵⁴¹ V⁵⁴³ M⁵⁴⁵ H⁵⁴⁷ N⁵⁴⁹ Y⁵⁵¹ H⁵⁵³ T⁵⁵⁵ P⁵⁵⁷ V⁵⁵⁹ V⁵⁶¹ P⁵⁶³ V⁵⁶⁵ S⁵⁶⁷ V⁵⁶⁹ M⁵⁷¹ H⁵⁷³ N⁵⁷⁵ Y⁵⁷⁷ H⁵⁷⁹ T⁵⁸¹ P⁵⁸³ V⁵⁸⁵ V⁵⁸⁷ P⁵⁸⁹ V⁵⁹¹ S⁵⁹³ V⁵⁹⁵ M⁵⁹⁷ H⁵⁹⁹ N⁶⁰¹ Y⁶⁰³ H⁶⁰⁵ T⁶⁰⁷ P⁶⁰⁹ V⁶¹¹ V⁶¹³ P⁶¹⁵ V⁶¹⁷ S⁶¹⁹ V⁶²¹ M⁶²³ H⁶²⁵ N⁶²⁷ Y⁶²⁹ H⁶³¹ T⁶³³ P⁶³⁵ V⁶³⁷ V⁶³⁹ P⁶⁴¹ V⁶⁴³ S⁶⁴⁵ V⁶⁴⁷ M⁶⁴⁹ H⁶⁵¹ N⁶⁵³ Y⁶⁵⁵ H⁶⁵⁷ T⁶⁵⁹ P⁶⁶¹ V⁶⁶³ V⁶⁶⁵ P⁶⁶⁷ V⁶⁶⁹ S⁶⁷¹ V⁶⁷³ M⁶⁷⁵ H⁶⁷⁷ N⁶⁷⁹ Y⁶⁸¹ H⁶⁸³ T⁶⁸⁵ P⁶⁸⁷ V⁶⁸⁹ V⁶⁹¹ P⁶⁹³ V⁶⁹⁵ S⁶⁹⁷ V⁶⁹⁹ M⁷⁰¹ H⁷⁰³ N⁷⁰⁵ Y⁷⁰⁷ H⁷⁰⁹ T⁷¹¹ P⁷¹³ V⁷¹⁵ V⁷¹⁷ P⁷¹⁹ V⁷²¹ S⁷²³ V⁷²⁵ M⁷²⁷ H⁷²⁹ N⁷³¹ Y⁷³³ H⁷³⁵ T⁷³⁷ P⁷³⁹ V⁷⁴¹ V⁷⁴³ P⁷⁴⁵ V⁷⁴⁷ S⁷⁴⁹ V⁷⁵¹ M⁷⁵³ H⁷⁵⁵ N⁷⁵⁷ Y⁷⁵⁹ H⁷⁶¹ T⁷⁶³ P⁷⁶⁵ V⁷⁶⁷ V⁷⁶⁹ P⁷⁷¹ V⁷⁷³ S⁷⁷⁵ V⁷⁷⁷ M⁷⁷⁹ H⁷⁸¹ N⁷⁸³ Y⁷⁸⁵ H⁷⁸⁷ T⁷⁸⁹ P⁷⁹¹ V⁷⁹³ V⁷⁹⁵ P⁷⁹⁷ V⁷⁹⁹ S⁸⁰¹ V⁸⁰³ M⁸⁰⁵ H⁸⁰⁷ N⁸⁰⁹ Y⁸¹¹ H⁸¹³ T⁸¹⁵ P⁸¹⁷ V⁸¹⁹ V⁸²¹ P⁸²³ V⁸²⁵ S⁸²⁷ V⁸²⁹ M⁸³¹ H⁸³³ N⁸³⁵ Y⁸³⁷ H⁸³⁹ T⁸⁴¹ P⁸⁴³ V⁸⁴⁵ V⁸⁴⁷ P⁸⁴⁹ V⁸⁵¹ S⁸⁵³ V⁸⁵⁵ M⁸⁵⁷ H⁸⁵⁹ N⁸⁶¹ Y⁸⁶³ H⁸⁶⁵ T⁸⁶⁷ P⁸⁶⁹ V⁸⁷¹ V⁸⁷³ P⁸⁷⁵ V⁸⁷⁷ S⁸⁷⁹ V⁸⁸¹ M⁸⁸³ H⁸⁸⁵ N⁸⁸⁷ Y⁸⁸⁹ H⁸⁹¹ T⁸⁹³ P⁸⁹⁵ V⁸⁹⁷ V⁸⁹⁹ P⁹⁰¹ V⁹⁰³ S⁹⁰⁵ V⁹⁰⁷ M⁹⁰⁹ H⁹¹¹ N⁹¹³ Y⁹¹⁵ H⁹¹⁷ T⁹¹⁹ P⁹²¹ V⁹²³ V⁹²⁵ P⁹²⁷ V⁹²⁹ S⁹³¹ V⁹³³ M⁹³⁵ H⁹³⁷ N⁹³⁹ Y⁹⁴¹ H⁹⁴³ T⁹⁴⁵ P⁹⁴⁷ V⁹⁴⁹ V⁹⁵¹ P⁹⁵³ V⁹⁵⁵ S⁹⁵⁷ V⁹⁵⁹ M⁹⁶¹ H⁹⁶³ N⁹⁶⁵ Y⁹⁶⁷ H⁹⁶⁹ T⁹⁷¹ P⁹⁷³ V⁹⁷⁵ V⁹⁷⁷ P⁹⁷⁹ V⁹⁸¹ S⁹⁸³ V⁹⁸⁵ M⁹⁸⁷ H⁹⁸⁹ N⁹⁹¹ Y⁹⁹³ H⁹⁹⁵ T⁹⁹⁷ P⁹⁹⁹ V¹⁰⁰¹ V¹⁰⁰³ P¹⁰⁰⁵ V¹⁰⁰⁷ S¹⁰⁰⁹ V¹⁰¹¹ M¹⁰¹³ H¹⁰¹⁵ N¹⁰¹⁷ Y¹⁰¹⁹ H¹⁰²¹ T¹⁰²³ P¹⁰²⁵ V¹⁰²⁷ V¹⁰²⁹ P¹⁰³¹ V¹⁰³³ S¹⁰³⁵ V¹⁰³⁷ M¹⁰³⁹ H¹⁰⁴¹ N¹⁰⁴³ Y¹⁰⁴⁵ H¹⁰⁴⁷ T¹⁰⁴⁹ P¹⁰⁵¹ V¹⁰⁵³ V¹⁰⁵⁵ P¹⁰⁵⁷ V¹⁰⁵⁹ S¹⁰⁶¹ V¹⁰⁶³ M¹⁰⁶⁵ H¹⁰⁶⁷ N¹⁰⁶⁹ Y¹⁰⁷¹ H¹⁰⁷³ T¹⁰⁷⁵ P¹⁰⁷⁷ V¹⁰⁷⁹ V¹⁰⁸¹ P¹⁰⁸³ V¹⁰⁸⁵ S¹⁰⁸⁷ V¹⁰⁸⁹ 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Figure 27

hBR96-2A: Heavy Chain Variable Region (V_H)

1 11 21 31 41
EVQLVESGGG LVQPGGSLRL SCAASGFPFS DYYMYWVRQA PGKGLEWVSY
51 61 71 81 91
ISQDGDITDY ADSVKGRFTI SRDNAKNSLY LQMNSLRDED TAVYYCARGL
101 111
ADGAWFAYWG QGTLVTVSS (SEQ ID NO. 24)

hBR96-2A: Human Heavy Chain IgG1 Constant Region $\Delta CH2$

A STKGPSVFPL APSSKSTSGG DAALGCLVKD YFPEPVTVSW NSGALTSGVH
TFPAVLQSSG LYSLSSVVTV PSSSLGTQTY ICNVNHKPSN TKVDKKVEPK
SCDKTHTCPP CP GOPREPQV YTLPPSRDEL TKNQVSLTCL VKGFYPSDIA
VEWESNGQPE NNYKTPPPVLDSDGSFFLYS KLTVDKSRWQ QGNVFSC9VM
HEALHNHYTQ KSLSLSPGK (SEQ ID NO. 26)

Figure 28

This sequence is the chi BR95 IgG1 with CH2 deleted.

1 VH EVNLVESGGG LVQPGGSLKV SCVTSGFTFS DYMYWVRQT PEKRLEWVAY
51 ISQGGDITDY PDTVKGRFTI SRDNAKNTLY LQMSRLKSED TAMYYCARGL
101 DDGAWFAYWG QGTLVTVSVA ^{CH1} STKGPSVFPL APSSKSTSGG TAALGCLVKD
151 YFPEPVTVSW NSGALTSGVH TFPAVLQSSG LYSLSSVVTV PSSSLGTQTY
201 ICNVNHKPSN TKVDKKVEPK SCDKTHTCPP ^{CH2} CGQPREPQV YTLPPSRDEL
251 TKNQVSLTCL VKGFYPSDIA VEWESNGQPE NNYKTPPPVL DSDGSFFLYS
301 KLTVDKSRWQ QGNVFSCSVM HEALHNHYTQ KSLSLSPGK

(SEQ ID NO. 27)